

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 11:57:46 ; Search time 4373 Seconds  
(without alignments)  
10604.080 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 95/  
Sequence: 1 atgatgagaccacatggt.....caagtggtggaacacttga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Database :

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8:  gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	956.6	100.0	957	9	AY724955	AY124955 Homo sapi
5	956.6	100.0	72045	9	AC092214	AC092214 Homo sapi
6	953.6	99.6	954	6	BD11274	BD11274 Novel G p
7	953.6	99.6	954	6	BD18556	BD18556 Novel G p
8	941.8	98.4	957	9	AY72486	AY72486 Pan panis
9	940.6	98.3	957	9	AY72491	AY72491 Pan trogl
10	932.2	97.4	957	9	AY72493	AY72493 Gorilla g
11	892.6	93.3	957	9	AY72496	AY72496 Pongo pyg
12	875	91.4	957	9	AY75022	AY75022 Macaca mu
13	524.6	54.8	203639	2	AC11765	AC11765 Mus muscu
14	514.6	53.8	966	10	AF532786	AF532786 Mus muscu
15	507	52.1	218921	2	AC097912	AC097912 Rattus no
16	498.6	52.1	966	10	AY362748	AY362748 Rattus no
17	296	30.9	13155	2	AC14312	AC14312 Macaca mu
18	249.8	26.1	924	6	BD144615	BD144615 Novel G-p
19	249.8	26.1	924	6	CQ738419	CQ738419 Sequence

20	249.8	26.1	924	9	AY144093	AY144093	Homo sapi
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22	249.8	26.1	175228	2	AC133333	AC143343	Homo sapi
23	249.8	26.1	200123	9	AC073284	AC073284	Homo sapi
24	248.2	25.9	924	9	AY724891	AY724891	Pan trogl
25	246.6	25.8	921	6	C0800004	C0800004	Sequence
26	246.6	25.8	924	9	AF644232	AF644232	Homo sapi
27	246.6	25.8	924	9	AY724956	AY724956	Homo sapi
28	243.4	25.4	924	9	AY724869	AY724869	Pan panis
29	241.6	25.2	924	9	AY724987	AY724987	Pongo pyg
30	239.8	25.1	924	9	AY724933	AY724933	Gorilla g
31	232.2	24.3	924	9	AY725013	AY725013	Macaca mu
32	230.2	24.1	924	9	AY724831	AY724831	Papio ham
33	214.8	22.4	3347	6	AX097850	AX097850	Sequence
34	192.4	20.1	927	6	AF240768	AF240768	Rattus no
35	192.4	20.1	1285	6	AX097794	AX097794	Sequence
36	190.8	19.9	223179	2	AC128080	AC128080	Rattus no
37	18.6	14.5	885	10	AY362747	AY362747	Rattus no
38	129	13.5	939	9	AY724864	AY724864	Pan panis
39	127.4	13.3	939	9	AY724931	AY724931	Gorilla g
40	125.8	13.1	939	9	AY724899	AY724899	Pan trogl
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## ALIGNMENTS

[illegible]



LOCUS AY114094 957 bp DNA linear PRI 28-FEB-2003  
DEFINITION Homo sapiens putative taste receptor T2R60 gene, complete cds.  
ACCESSION AY114094  
VERSION AY114094.1 GI:28603637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 957)  
Conte,C., Ebeling,M., Marcuz,A., Nef,P. and Andres-Barquin,P.J.  
TITLE Identification and characterization of human taste receptor genes  
belonging to the T2R family  
JOURNAL Cytogenet. Genome Res. 98 (1), 45-53 (2002)  
MEDLINE 22472936  
PubMed 12584440  
2 (bases 1 to 957)  
Conte,C., Ebeling,M., Marcuz,A., Nef,P. and Andres-Barquin,P.J.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche  
Ltd., Grenzacherstrasse 124, Basel CH-4070, Switzerland  
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Best Local Similarity 99.9%; Pred. No. 3.6e-284;  
Matches 956; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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ACCESSION AY724955  
VERSION AY724955.1 GI:51989208  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 957)  
Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany  
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## ORIGIN

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Query Match 100.0%; Score 956.6; DB 9; Length 957;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-284;  
 Matches 957; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGAGACCAATGTTCTAGAGTCTTCGGTGTGACAGCAAGAGCCATCATCTTG 60  
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 QY 61 GTTACATTTTACTCTTTTACGCTGTGAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
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 QY 121 GCTCTGGGCGTGTGAGTGGTGTGACGAGAAATGTTGCTCTGTGATTAATGTTGTT 180  
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 1 (bases 1 to 72045)  
 Hillier, L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H.,  
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 Fowell, G.A., Delhanty, K.D., Miner, T.L., Nash, M.E., Cordes, M.,  
 Du, R., Sun, H., Edwards, J., Bradshaw-Cordum, H., Ali, J., Andrews, S.,  
 Isak, A., Vanbrunt, A., Nguyen, C., Du, F., Lamar, B., Courtney, L.,  
 Kallio, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A.,  
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 Dauphin-Kohlberg, S., Kozlowicz-Reilly, A., Leonard, S., Rohlfing, T.,  
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 Strommatt, C., Latreille, P., Miller, N., Johnson, D., Murray, J.,  
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 Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A.,  
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 Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Torrens, D.,  
 Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V.,  
 Eichler, E.E., Green, E.D., Waterston, R.H. and Wilson, R.K.  
 The DNA sequence of human chromosome 7  
 Nature 424 (6945), 157-164 (2003)  
 JOURNAL  
 MEDLINE  
 22737999  
 PUBMED  
 12853948  
 REFERENCE  
 Doeber, A., Elliott, G., Kozlowicz, A. and Sun, H.  
 The sequence of Homo sapiens BAC clone RP11-811J9  
 Unpublished (2001)  
 JOURNAL  
 3 (bases 1 to 72045)  
 REFERENCE  
 Waterston, R.H.  
 Direct Submission  
 Submitted (29-JUN-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE  
 4 (bases 1 to 72045)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (15-NOV-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
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 5 (bases 1 to 72045)  
 Waterston, R.H.  
 Direct Submission  
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 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
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 6 (bases 1 to 72045)  
 Waterston, R.  
 Direct Submission  
 Submitted (10-JAN-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 REFERENCE  
 7 (bases 1 to 72045)  
 Wilson, R.  
 Direct Submission  
 Submitted (31-JAN-2004) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Nov 15, 2001 this sequence version replaced gi:15625026.  
 COMMENT  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center



Center code: MUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
----- Summary Statistics -----  
Center project name: H\_NH0811J09  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Fritgen, R., Tatem, M., Catanesi, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-563K23 the clone sequenced to the right is RP11-298A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-811J9 actual end is at base position 140619 of RP11-298A10.

Location/Qualifiers

#### FEATURES

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DB 62877 GTTACATTTTACTCTTTTACGCTGTGAGCAATGACGAGCAATGAGCTTCATCAGTCT 62936

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DB 62937 GCTCTGGCGTGGAGTGGTGTCTACGAGAAATGTTGCTTGTGATAATTATGTT 62996

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BD171274 954 bp DNA linear PAT 17-JAN-2003
LOCUS Novel G protein-coupled receptor protein and DNA thereof.
DEFINITION BD171274
ACCESSION BD171274
VERSION 1.0
KEYWORDS G protein-coupled receptor protein and DNA thereof
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 954)
Molecular Weight: 102558 Da
Accession Number: U00002.1
Gene Name: GPR108
Gene ID: 10814
Gene Symbol: GPR108
Gene Description: Novel G protein-coupled receptor protein and DNA thereof
Gene Source: TAKEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, TAKASHI ITO, YASUSHI
SHINJANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
PN WO 02057309-A/1

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PD 25-JUL-2002
PF 17-JAN-2002 WO 2002JP000271
PR 18-JAN-2001 JP 01P 010814.10-MAR-2001 JP 01P 102558 PI
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C07K16/28,
PC C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC
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Key Location/Qualifiers
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QY 241 TTCTTGATCCGATGGCTTCCCATACACCTCTGACTGAGTTTCTAGTTTCCAGTGG 300
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Db	721	GCACACATPAAGGCTCTGCTGAGCTCTCCTCTCTTTTGGCAGTCTTTCATCTCATATTTC	780
Qy	781	CTGTACCTGGTGTTCAGTGTGACAGGTATTTTTCACACTCTGAACTTTAAATTCGGGTG	840
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Qy	841	TGGGAGTACGATGATTTATCTGTGTGTCAGCAGTTCACCCCATCATCTCTCTTCAGCAAC	900
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DEFINITION	Novel G protein-coupled receptor and its DNA.		
ACCESSION	BD185566		
VERSION	BD185566.1	GI:31877766	
KEYWORDS	JP 2002360279-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 954)		
TITLE	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.		
JOURNAL	Novel G protein-coupled receptor and its DNA		
COMMENT	Patent: JP 2002360279-A 1 17-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD		
	OS Homo sapiens (human)		
	PN JP 2002360279-A/1		
	PD 17-DEC-2002		
	PF 17-JAN-2002 JP 2002008445		
	PI MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA		
	PC C12N15/09, A61K39/395, A61K39/395, A61K45/00, A61P1/00, A61P3/00,		
	PC A61P5/00,		
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Qy	181	AGCCTAAGGGGCTTCGCTTCTGTCTGCAAGTCAAGTGTAAATGGGTAAACCAATTATGTT	240	
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Qy	241	TTCTTTGCATCCGATGGGCTTCCCTAACAACCTGTATGCAAGTTTCTAGCTTTCAGATGG	300	
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Qy	301	GACTTCCTGAAATGCTGGCACTTATGGTCCCTACCTGAGCTCAAGTCTTATTTGTGTG	360	
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Qy	361	AAAATTGCTACCTTCAACCAACCCGTCTTCTTCTGCTAAAGCAACAAGTGTCTGGGTGG	420	
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Qy	421	CTACCATGATGCTCTTCTCAGCTCTGTAGGGGCTCTCCAGCTTACACCACTTCTATTTTTC	480	
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Qy	481	ATTAGCAACCAAGAAATGATCAGAACTATTATAGAAACATCTACAACCTGGATGTG	540	
Db	481	ATTAGCAACCAAGAAATGATCAGAACTATTATAGAAACATCTACAACCTGGATGTG	540	
Qy	541	ACTGGCGATAGCATACGAGAGCTACTGTGAGAAATTTATCTCTTCCCTCTAAAAATGAT	600	
Db	541	ACTGGCGATAGCATACGAGAGCTACTGTGAGAAATTTATCTCTTCCCTCTAAAAATGAT	600	
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DEFINITION	Pan paniscus chromosome 7 taste receptor 12R56 gene, complete cds.			
ACCESSION	AY724866			
VERSION	AY724866.1	GI:51989057		
KEYWORDS				
SOURCE				
ORGANISM	Pan paniscus (pygmy chimpanzee)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.			
TITLE	Anne, F., Yoav, G., Orn, M. and Svante, P.			
JOURNAL	Evolution of bitter taste receptors in human and apes			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 957)			
	Anne, F., Yoav, G., Orn, M. and Svante, P.			

TITLE	Direct Submission
JOURNAL	Submitted (12-AUG-2004) Genetics, Max-Planck Institute for

FEATURES	Location/Qualifiers
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CDS	1.1957
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## ORIGIN

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Db	241	TTCTTGATC	CGAGAGGCTTCCCATACAACCTGTATCTGCAATTTCTAGCTTTCAGTGG	300
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Oy	481	ATAGGCA	CCACAGATGATTCAGAACTATTTAAGAACATCTTCAACCTTGGAAATGTC	540
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Db	66.	GGAAAGACATGAMAGGCTCTCCTTCAACCTCAGGATTCGAGAGCCAGGTGACG	720
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LOCUS	AY724901
DEFINITION	AY724901 957 bp DNA linear PRI 18-SEP-2000
ACCESSION	Pan troglodytes chromosome 7 taste receptor 12R56 gene, complete cds.
VERSION	AY724901
KEYWORDS	AY724901.1 GI:51989117
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes  
Unpublished  
2 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Direct Submission  
Submitted (12-AUG-2004) Genetics, Max-Planck Institute for

CDS

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			PRI 18-SEP-2004
ACCESSION	AY724986		
VERSION	AY724986.1		
KEYWORDS	GI:51989260		
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ORGANISM	Pongo pygmaeus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Pongo.		
REFERENCE	1 (bases 1 to 957)		
AUTHORS	Anne,F., Yoav,G., Orna,M. and Svante,P.		
TITLE	Evolution of bitter taste receptors in human and apes		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 957)		
AUTHORS	Anne,F., Yoav,G., Orna,M. and Svante,P.		
TITLE	Direct Submission		
JOURNAL	Submitted (12/AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany		

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ORIGIN	Query Match	93.3%	Score 892.6	DB 9	Length 957
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RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
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							Macaca mulatta (rhesus monkey)			
							Macaca mulatta			
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Macaca.			
							1 (bases 1 to 957)			
							Anne,F., Yoav,G., Orna,M. and Svante,P.			
							Evolution of bitter taste receptors in human and apes			





Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicoli, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (13-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 13, 2004 this sequence version replaced gi:37591301.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information

Center Project name: L23370  
Center Clone name: 115\_M.13  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 202836 bases at least Q40  
Consensus quality: 203382 bases at least Q30  
Consensus quality: 203644 bases at least Q20  
Insert size: 198000; agarose-fp  
Insert size: 203825; sum-of-coverage  
Quality coverage: 10.9 in Q20 bases; agarose-fp  
Quality coverage: 10.6 in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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CC The present sequence encodes human bitter taste receptor T2R72. The human  
CC T2R72 gene is located on chromosome 7 in the region 1440626592-144063548.  
CC The reading frame of T2R72 is intronless. T2R72 polypeptides and  
CC polymorphs are useful for identifying modulators. Such modulators  
CC are useful for modulating bitter taste perception in a subject. T2R72  
CC agonists can be administered to enhance bitter tastes, while T2R72  
CC antagonists can be administered to reduce bitter taste.

SQ Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;

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Matches 956; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

ID ADM33336 standard; cDNA; 957 BP

AC ADM3336;

DT 18-NOV-2004 (first entry)

DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.

**KW** human; bitter taste receptor; food; gene; ss.

**Homo sapiens**

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DR P-PSDB; ADM33335

PT Novel bitter receptor polynucleotide encoding human TAS2R protein having

PT pharmaceutical compositions comprising antagonists of bitter taste

XXXX

XX

CC The present sequence encodes a human bitter taste receptor. Also  
CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
CC a vector (II) containing (I); (3) a host cell (III) genetically  
CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
CC acid sequence encoded by (I) or obtained by culturing (III) and  
CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
CC isolating (M1) a compound that binds to (V) encoded by (I); (10)  
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
CC foodstuff including human and animal foodstuff, any precursor material or  
CC additive employed in the production of foodstuff comprising (VIII); and  
CC (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an  
CC active agent and optionally a carrier. (III) is useful for producing a  
CC polypeptide encoded by (I), which involves culturing (III) and recovering  
CC the polypeptide encoded by (I). (II) is useful for producing cells  
CC capable of expressing at least one of the bitter taste receptor  
CC polypeptide, which involves genetically cells in vitro with (I), where  
CC the bitter taste receptor polypeptide(s) is (are) encoded by (I). (M1) or  
CC (M2) can be used for producing food or any precursor material or additive  
CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
CC for producing nutraceutical or pharmaceutical compositions. (I), (II),  
CC (VI) or (VIII) can be used for manufacturing a medicament for the  
CC treatment of an abnormally increased or decreased sensitivity towards a

CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminated bitter tasting components of food and effectively useful in  
CC food industries.

XX Sequence 957 BP; 203 A; 240 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 100.0%; Score 956.6; DB 13; Length 957;  
Best Local Similarity 99.9%; Pred. No. 1.8e-292;  
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DB 421 CTACCATGATGCTCTTCAAGTCTGTAGAGGCTCTCCACGCTTCAACACCATTTATTTTC 480
QY 481 ATAGGCAACCAACAATGATACAGATCTTAAAGAACATCTAACACCTTGAATGTC 540
DB 481 ATAGGCAACCAACAATGATACAGATCTTAAAGAACATCTAACACCTTGAATGTC 540
QY 541 ACTGGCATAGCATACGAGAGCTACTGTAGAAATTTATCTCTTCCCTTAAATGATT 600
DB 541 ACTGGCATAGCATACGAGAGCTACTGTAGAAATTTATCTCTTCCCTTAAATGATT 600
QY 601 ACTTGAACAATGCCCACTGCTGCTTTTTCATTTGATGATTTTGTCTCATCACTCTG 660
DB 601 ACTTGAACAATGCCCACTGCTGCTTTTTCATTTGATGATTTTGTCTCATCACTCTG 660
QY 661 GGAAGACACAGGAAGAGGCTCTCTTACAACCTCAGGATCCGAGAGCCAGAGTGCAG 720
DB 661 GGAAGACACAGGAAGAGGCTCTCTTACAACCTCAGGATCCGAGAGCCAGAGTGCAG 720
QY 721 GCACACATAAAGGCTGCTGCTCTCTCTCTTTTGGCATGCTCTTATCTCATATTTTC 780
DB 721 GCACACATAAAGGCTGCTGCTCTCTCTCTCTTTTGGCATGCTCTTATCTCATATTTTC 780
QY 781 CTGTCACTGCTGTTCACTGCTGACAGATTTTTCACCTCTGGAATTTTAAATTCGGGTC 840
DB 781 CTGTCACTGCTGTTCACTGCTGACAGATTTTTCACCTCTGGAATTTTAAATTCGGGTC 840
QY 841 TGGAGTCAGTGAATTTATCTGTGTCAGACAGTTTACCCCATCATTTGCTCTTACGACAC 900
DB 841 TGGAGTCAGTGAATTTATCTGTGTCAGACAGTTTACCCCATCATTTGCTCTTACGACAC 900
QY 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGCCTTCTCAAGTGTGGGACACCTTGA 957
DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGCCTTCTCAAGTGTGGGACACCTTGA 957

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## RESULT 3

ABK87584  
ID ABK87584 standard; cDNA; 954 BP.

AC ABK87584;

DT 24-SEP-2002 (first entry)

XX DNA encoding novel human G-protein coupled receptor.

XX G-protein coupled; receptor; liver; central nervous system disease;  
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;  
XX hyperlipaemia; cancer; non-small cell lung cancer; ovarian cancer;  
XX stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;  
XX circulatory disease; hypertension; atherosclerosis; angina; allergy;  
XX inflammatory disease; respiratory disease; asthma; bronchitis;  
XX digestive disease; stomach ulcer; duodenal ulcer; immune disorder;  
XX autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;  
XX pneumonia; influenza; gene; 95.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX Key 1.954  
XX CDS /tag= a  
XX /product= "Novel G-protein coupled receptor"  
XX /partial  
XX /note= "No stop codon given"

XX W0200257309-A1.

XX 25-JUL-2002.

XX 17-JAN-2002; 2002MO-JP000271.

XX 16-JAN-2001; 2001JP-00010814.

XX 30-MAR-2001; 2001JP-00102558.

XX (TAKA ) TAKEDA CHEM IND LTD.

XX Miwa M, Ito T, Shintani Y, Miyajima N;

XX WPI; 2002-538457/57.

XX P-PSDB; AAU98514.

XX New G-protein coupled receptor protein expressed in human liver for  
XX design of drugs and reagents for treatment and diagnosis of cancer and  
XX respiratory metabolic and other diseases.

XX Claim 6; Page 91; 101pp; Japanese.

XX The invention describes a novel G-protein coupled receptor protein  
XX expressed in human liver. The protein is used in the treatment,  
XX prevention and diagnosis of central nervous system diseases (such as  
XX Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes  
XX and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
XX cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
XX inflammatory diseases (such as hypertension, atherosclerosis and angina),  
XX inflammatory diseases (such as allergy and rheumatism), respiratory  
XX diseases (such as asthma and bronchitis), digestive diseases (such as  
XX stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
XX diseases), and infections (such as acquired immunodeficiency syndrome  
XX (AIDS), pneumonia and influenza). This sequence encodes the novel G-  
XX protein coupled receptor protein described in the invention

XX Sequence 954 BP; 202 A; 241 C; 214 G; 297 T; 0 U; 0 Other;

Query Match 99.6%; Score 953.6; DB 6; Length 954;  
Best Local Similarity 99.9%; Pred. No. 1.6e-291;  
Matches 953; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGATGAGAGACCATGTTCTAGAGATCTTCGGTGAAGTGAAGAGGCCATCATCTTG 60
Db 1 ATGATGAGAGACCATGTTCTAGAGATCTTCGGTGAAGTGAAGAGGCCATCATCTTG 60
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Db 61 GTTACCATTTTACTCCCTTTTAAAGCTGTGTGCAATAGCAGGCAATGGCTTCAATCACTGCT 120
QY 121 GCTGGGCGGTGAGTGGGTGTCTACGGAGATGTGTGTGCTGTGTGATTAAGTTATGGT 180
Db 121 GCTGGGCGGTGAGTGGGTGTCTACGGAGATGTGTGTGCTGTGTGATTAAGTTATGGT 180
QY 181 AGCCTAGAGGGCCTCTGCTCTCTGTCTGCACTAGTGTGTAATGGGTAAAGACATTTATGTT 240
Db 181 AGCCTAGAGGGCCTCTGCTCTCTGTCTGCACTAGTGTGTAATGGGTAAAGACATTTATGTT 240
QY 241 TTCTTGATCCGATGGCTTCCCTATACACCCTGTACTGCAATTTCAAGCTTTCAGTGG 300
Db 241 TTCTTGATCCGATGGCTTCCCTATACACCCTGTACTGCAATTTCAAGCTTTCAGTGG 300
QY 301 GACTTCCTGAATGCTGCGACCTTATGGTCTCTACCTGAGTGTCTTCTATATGTTG 360
Db 301 GACTTCCTGAATGCTGCGACCTTATGGTCTCTACCTGAGTGTCTTCTATATGTTG 360
QY 361 AAAATTGCTACCTTCAACCCACCCCTGTCTTCTGTGCTAAAGCAAGATTGCTGGGTGG 420
Db 361 AAAATTGCTACCTTCAACCCACCCCTGTCTTCTGTGCTAAAGCAAGATTGCTGGGTGG 420
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Db 421 CTACCATGATGCTCTTCACTCTGTGAGGGCTCTCCAGCTTACACCACTTCTATTTTTC 480
QY 481 ATAGGCAACCAAGATGTATCAGAACTATTTAAGAAACATCTACAACCTTGAATGTC 540
Db 481 ATAGGCAACCAAGATGTATCAGAACTATTTAAGAAACATCTACAACCTTGAATGTC 540
QY 541 ACTGGCGATGACATACGAGACTCTGTGAGAAATTTATCTCTCCCTCTAAAAATGAT 600
Db 541 ACTGGCGATGACATACGAGACTCTGTGAGAAATTTATCTCTCCCTCTAAAAATGAT 600
QY 601 ACTTGGACATGCCCACATGCTGTCTTTTTCATTTGCAATTTTGTCTATCAATCTCTG 660
Db 601 ACTTGGACATGCCCACATGCTGTCTTTTTCATTTGCAATTTTGTCTATCAATCTCTG 660
QY 661 GGAAGACACAGAAAGAGCTCTCTTACAACCTCAGAAATCCGAGAGCCAGTGTGAG 720
Db 661 GGAAGACACAGAAAGAGCTCTCTTACAACCTCAGAAATCCGAGAGCCAGTGTGAG 720
QY 721 GCAACATTAAGGCTGTGCTGTCTCTCTCTTTTGCATGCTTTCATCTCATATTTC 780
Db 721 GCAACATTAAGGCTGTGCTGTCTCTCTCTTTTGCATGCTTTCATCTCATATTTC 780
QY 781 CTGTCACTGTGTCTGATGCTGTGCAAGTATTTTTCACACTCTGCACTTAAATCTGGGTG 840
Db 781 CTGTCACTGTGTCTGATGCTGTGCAAGTATTTTTCACACTCTGCACTTAAATCTGGGTG 840
QY 841 TGGAGTCACTGATTTATCTGTGTGAGAGATTCAACCCATCAATTTCTGCTTTCAGAGAC 900
Db 841 TGGAGTCACTGATTTATCTGTGTGAGAGATTCAACCCATCAATTTCTGCTTTCAGAGAC 900
QY 901 TGCAGGCTGAGAGCTGTGTGTAAGAGTGTGTCTCTCAAGGTGTGGAGACCT 954
Db 901 TGCAGGCTGAGAGCTGTGTGTAAGAGTGTGTCTCTCAAGGTGTGGAGACCT 954
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RESULT 4  
ACC44449 standard; DNA; 939 BP.

XX ACC44449;  
XX  
DT 25-JUL-2003 (first entry)  
XX

```
DE Gene encoding mouse GI endocrine cell specific GPCR GTR2-m39.  
XX  
XX Chemosensor; G-protein coupled receptor; gene; de; GPCR; receptor;  
KM gastrointestinal tract; taste; ion channel; enteroendocrine cell.  
OS Mus musculus.  
PN M02003031604-A1.  
PD 17-APR-2003.  
PF 11-OCT-2002; 2002MO-US032664.  
PR 12-OCT-2001; 2001US-0328993P.  
PA (REGC) UNIV CALIFORNIA.  
PI (PHLE/) PHELEGER C S W.  
PI Walsh JH, Rozenfurt JE, Wu SV;  
XX WPI; 2003-381713/36.  
DR P-PSDB; ABR58013.  
XX  
XX New nucleic acid encoding a chemosensing G-protein coupled receptor,  
PT useful for identifying chemical sensing receptors and signaling molecules  
PT that allow pharmacological and genetic modulation of taste transduction  
PT pathways.  
XX  
PS Claim; Page 63; 101pp; English.  
XX  
XX This sequence represents a gene encoding a novel isolated chemosensing G-  
CC protein coupled receptor (GPCR) from the gastrointestinal tract. The  
CC nucleic acid is useful for identifying or isolating chemical sensing  
CC receptors (including taste ion channels) and signaling molecules that  
CC would allow pharmacological and genetic modulation of taste transduction  
CC pathways. The native STC-1 enteroendocrine cells that naturally express  
CC GTR2 are useful in identifying modulators of taste receptor-mediated  
CC signal transduction. These cells are also used as models for studying  
XX taste-mediated signal transduction  
XX  
SQ Sequence 939 BP; 224 A; 209 C; 202 G; 304 T; 0 U; 0 Other;  
Query Match 53.8%; Score 514.6; DB 8; Length 939;  
Best Local Similarity 71.7%; Pred. No. 3,6e-152;  
Matches 673; Conservative 1; Mismatches 265; Indels 0; Gaps 0;  
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QY 61 GTTACCATTTTACTCCCTTTTAAAGCTGTGTGCAATAGCAGGCAATGGCTTCAATCACTGCT 120  
Db 61 GTTACCATTTTACTCCCTTTTAAAGCTGTGTGCAATAGCAGGCAATGGCTTCAATCACTGCT 120  
QY 121 GCTGGGCGGTGAGTGGGTGTCTACGGAGATGTGTGTGCTGTGTGATTAAGTTATGGT 180  
Db 121 GCTGGGCGGTGAGTGGGTGTCTACGGAGATGTGTGTGCTGTGTGATTAAGTTATGGT 180  
QY 181 AGCCTAGAGGGCCTCTGCTCTCTGTCTGCACTAGTGTGTAATGGGTAAAGACATTTATGTT 240  
Db 181 AGCCTAGAGGGCCTCTGCTCTCTGTCTGCACTAGTGTGTAATGGGTAAAGACATTTATGTT 240  
QY 241 TTCTTGATCCGATGGCTTCCCTATACACCCTGTACTGCAATTTCAAGCTTTCAGTGG 300  
Db 241 TTCTTGATCCGATGGCTTCCCTATACACCCTGTACTGCAATTTCAAGCTTTCAGTGG 300  
QY 301 GACTTCCTGAATGCTGCGACCTTATGGTCTCTACCTGAGTGTCTTCTATATGTTG 360  
Db 301 GACTTCCTGAATGCTGCGACCTTATGGTCTCTACCTGAGTGTCTTCTATATGTTG 360  
QY 361 AAAATTGCTACCTTCAACCCACCCCTGTCTTCTGTGCTAAAGCAAGATTGCTGGGTGG 420  
Db 361 AAAATTGCTACCTTCAACCCACCCCTGTCTTCTGTGCTAAAGCAAGATTGCTGGGTGG 420
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.2	13.0	12226	4	US-09-949-016-12237
2	113.2	11.8	876	4	US-09-949-016-2342
3	113.2	11.8	4876	4	US-09-949-016-12790
4	113.2	11.8	4877	4	US-09-949-016-14084
5	111.6	11.7	876	4	US-09-393-634-65
6	111.6	11.7	876	4	US-09-949-016-1048
7	105.2	11.0	1463	4	US-09-393-634-6
8	86.4	9.0	939	4	US-09-393-634-52
9	80	8.4	951	4	US-09-393-634-40
10	80	8.4	951	4	US-09-949-016-2336
11	80	8.4	4951	4	US-09-949-016-14078
12	76.4	8.0	900	4	US-09-393-634-42
13	75.4	7.9	910	4	US-09-393-634-38
14	74.8	7.8	1331	4	US-09-393-634-2
15	74	7.7	954	4	US-09-393-634-48
16	74	7.7	957	4	US-09-949-016-3382
17	74	7.7	4957	4	US-09-949-016-15124
18	68.4	7.1	930	4	US-09-393-634-50
19	62.4	6.5	900	4	US-09-949-016-1071
20	62.4	6.5	900	4	US-09-949-016-12813
21	62.4	6.5	900	4	US-09-949-016-14027
22	62.4	6.5	4900	4	US-09-949-016-12813
23	62.4	6.5	4900	4	US-09-949-016-14027
24	62	6.5	601	4	US-09-949-016-38861
25	62	6.5	601	4	US-09-949-016-78195
26	58	6.1	900	4	US-09-393-634-36
27	57.8	6.0	250352	4	US-09-949-016-14724

C	28	57.4	6.0	601	4	US-09-949-016-108443	Sequence 108443, A
C	29	56	5.9	397	4	US-09-949-016-108442	Sequence 108442, A
C	30	54.4	5.7	601	4	US-09-393-634-73	Sequence 73, Appl
C	31	54.2	5.7	601	4	US-09-949-016-108441	Sequence 108441, A
C	32	52.8	5.5	7218	1	US-08-232-463-14	Sequence 14, Appl
C	33	51.6	5.4	601	4	US-09-949-016-108134	Sequence 108134, A
C	34	51.2	5.3	601	4	US-09-949-016-108481	Sequence 108481, A
C	35	50.8	5.3	601	4	US-09-949-016-108480	Sequence 108480, A
C	36	50.4	5.3	601	4	US-09-949-016-38510	Sequence 38510, A
C	37	50.4	5.3	601	4	US-09-949-016-80952	Sequence 80952, A
C	38	50.4	5.3	1361	4	US-09-393-634-14	Sequence 14, Appl
C	39	50.2	5.2	466	4	US-09-393-634-71	Sequence 71, Appl
C	40	50.2	5.2	1532	4	US-09-393-634-18	Sequence 18, Appl
C	41	48.8	5.1	601	4	US-09-949-016-108296	Sequence 108296, A
C	42	48.8	5.1	601	4	US-09-949-016-108237	Sequence 108237, A
C	43	48	5.0	903	4	US-09-393-634-63	Sequence 63, Appl
C	44	47.6	5.0	1739	4	US-09-393-634-16	Sequence 16, Appl
C	45	45.6	4.8	924	4	US-09-393-634-54	Sequence 54, Appl

## ALIGNMENTS

RESULT 1							
US-09-949-016-12237							
Sequence 12237, Application US/09949016							
Patent No. 6812339							
GENERAL INFORMATION:							
APPLICANT: VENTER, J. Craig et al.							
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED							
FILE REFERENCE: C0001307							
CURRENT FILING DATE: 2000-04-14							
PRIOR APPLICATION NUMBER: 60/241,755							
PRIOR FILING DATE: 2000-10-20							
PRIOR APPLICATION NUMBER: 60/237,768							
PRIOR FILING DATE: 2000-10-03							
PRIOR APPLICATION NUMBER: 60/231,498							
PRIOR FILING DATE: 2000-09-08							
NUMBER OF SEQ ID NOS: 207012							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 12237							
LENGTH: 12226							
TYPE: DNA							
ORGANISM: Human							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (1) .. (12226)							
OTHER INFORMATION: n = A,T,C or G							
US-09-949-016-12237							
Query Match							
Best Local Similarity 48.2%; Pred. No. 4,76-29;							
Matches 425; Conservative 0; Mismatches 438; Indels 18; Gaps 2;							
13.0%; Score 124.2; DB 4; Length 12226;							
QY	53	TCATCTGTTGTTACATTTTACTCTTTTACGCTGTGAGCAATGAGGCAATGCTTCA	112				
DB	7935	TGATCTTCATAGCATCTTTTGTCTGAGTCATTTGGTGGCAATCTGCAGATGATCTT	7994				
QY	113	TCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	172				
DB	7995	TGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	8054				
QY	173	TATGCTGTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	232				
DB	8055	TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	8114				
QY	233	TTTATGTTTCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	292				
DB	8115	TCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	8159				
QY	293	TCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	352				

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Db      8160 TCTTCTGGGACCTTTTCAATGCCCCCTCACTTGTGTTTACGCTTGTGCTTCTTCT
Qy      353 ATTGTGTAATATGTAACCTTCAACCACTGCTCTTCTTGGCTAAGACAAAGTGT
Db      8220 ACTGTGTAAGATCTCATCTTTCTCCACCCACCTTGCTGGCTGAAGGAGAACT
Qy      413 CTGGGTGGCTACCAATGATGCTCTTCACTGTAGGAGCTCTCCAGCTTCCACCAATTC
Db      8280 CTGGTTAGTGGCCCAAGCTGATCAAGGGCTCCGATCATCTGTGGCTGAAGTCAATCT
Qy      473 TATTTTCAATAGGCAACCAAGAAATGATCAAACTATTAAAGAACCATCTACACCTT
Db      8340 CATCAGCCACCTGGGAACATCTGTTTGTAGAGAAAGTCTCCCTGAGTTCTTACAGAA
Qy      533 GGAATGTCACCTGGGATAGCATAGGAGCTCTGAGAAATTTATCTCTCCCTCA
Db      8400 ACGAACTCTAGTTTAAAGATGAGGAGCTTATTCAG--CTCTACTTTTCTTTATG
Qy      593 AAATGATTACTTGGACAATGCCCATGCTGCTTTTCAATTGGATGATTTTGGCTATCA
Db      8457 AAGGTTTGTGTGTCGATCTGTCTCTCTCTTCTAGTGTCACTGTCTGTCTATAG
Qy      653 CATCTCTGGGAGACACAGAAAGGCTCTCTTACACCTCAGAAATCCGAGAGCCCA
Db      8517 TCTCATCTGTGCTGAGTGGGATGATGAGGAGCTCAGGCCGCCGCTGTATCCCA
Qy      713 GTGTGAGGACACATAAAGGCTGCTGCTCTCTCTCTTTTGGCATGCTTTCATCT
Db      8577 GCACCCAGGCTTACATAGGCTTTAAAGTACATCTTTCCCTCACTTCTGTATCAT
Qy      773 CATATTTCTGTCACTGTGTTCAGTGTGCTGAGGATTTTTCACCTCTGACCTTAAAT
Db      8637 TGTACTTCTGTCTGTTGCTTCTGTGTTGAATAATCAATTAACCTTCAAGATCAGTGC
Qy      833 TCTGGGTGGAGATCAGTATTTATCTGTGTGAGACAGTTACCCCATCATTTGCTCT
Db      8697 ACTGGGCTGTGTAGTGTATCTATCTATGCAACATCTGTGCTGACCTTACCGTCTGTGTC
Qy      893 TCAGCACTGAGGCTGAGAGCTGTGCTGAGAGTCTGCT 933
Db      8757 TGAAGAGCCCACTGAATAAGAGGCTTGAAGACATGCT 8797
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## RESULT 2

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US-09-949-016-2342
; Sequence 2342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CI.001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2342
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2342
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Query Match      11.8%; Score 113.2; DB 4; Length 876;
Best Local Similarity 49.3%; Pred. No. 3.6e-26;
Matches 431; Conservative 0; Mismatches 413; Indels 30; Gaps 4;
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Qy      53 TCATCTGTGTACCAATTTTACTCTTTTACGCTGTAGCAATAGCAGCAATGCTTCA
Db      23 TCTTCTTCATGATCATCTATGTGCTGTAGCTTGTGCAATTAATGTGACAGAGCCTAA
Qy      113 TCAGTGTGCTGTGGGTGGAGTGGTGTGTAGGAAATGTTGGCTTGTGATAGT
Db      83 TTGTGTGAGTGTGGGAGAGAAATGGCTGTGAATCAGAAAGCTGTGTGAGACATGA
Qy      173 TATTTGTTAGCCTAAGGGGCTCTGCTTCTGTCTGACAGTGTGATGGTAAAGCA
Db      143 TTCTCATACAGCTGGGATCTCTGCTTCTGTCTAGAGTGGGATCAATCTGAAATAT
Qy      233 TTTATGTTTCTTGATCCGATGAGCTTCCATACAACTCTGATGCACTTTCAGCTT
Db      203 TTGCTCCATTTTAAATTTAATTAATGATTTGCAAC-----TTAACAA
Qy      293 TCCAGTGGGACTCTGTAATGCTGCCACTTAATGTCCTTACTGCTGAGTGTCTTCT
Db      248 TCACCTGGGAATTTTAAATATCTTACATTTCTGTTAAACACTTGTCTTACGTTCT
Qy      353 ATTGTGTAATATGCTACCTTCAACCACTGCTCTTCTTGGCTAAAGCAAGTTGT
Db      308 ACTGCATCAAGTCTCTCTTTTACCCATACATCTTCTGTGCTGAGTGGAGAAATTT
Qy      413 CTGGGTGCTACCAATGAGTCTTTCAGCTTGTGTAGGCTCTTCAAGCTTCAACCAATTC
Db      368 TGAAGTTGTTCCCTGGATATTAATGAGGCTTCTGATGATTAATTTGTTAAATATCC
Qy      473 TATTTTCAATAGGCAACCAAGAAATGATACAAATTTAAAGAACCTTACAACTT
Db      428 CTTGAGCTATTTGGAATTTAATTCATTAATTAAGTACTACCAATGAGAGATCT--ACCAA
Qy      533 GGAATGTCAGTGGGATAGCATAGGAGTACTGTGAGAAATTTCTTCCCTCTAA
Db      485 GAAACAGACTGTATACGTGAACAACTTGAATTTTATCA--GTAACATTTCCAGGCTC
Qy      593 AAATGATTACTTGGACATGCCCACTGCTCTTTTTCATTTGCAATGATTTTGTCTATCA
Db      542 ATACAGTTGATGTTATTTCTTTTATCTGTTTCCGCTGCTCCACCATCTTTCTCATAG
Qy      653 CATCTCTGGGAAGACACAGAAAGGCTCTCTTACAACTCAGAAATTCGAGAGCCCA
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Qy      713 GTGTGAGGACACATTAAGGCTCTGCTGCTCTCTCTCTTTTGGCATGCTCTTCAATCT
Db      653 GCATGAAGGCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTTATTTATGTGTTAACT
Qy      773 CATATTTCTGTCACTGTGTGTTGAGTGTGAGGATTTTTCACCTCTGACCTTAAAT
Db      833 TCTGGGTGGAGATCAGTATTTATCTGTGTGAGACAGTTACCCCATCATTTGCTCT
Qy      833 TATGGGTCTGGAGGCTTTTGTCTATGCTTTCATTTAAATGATTCATCTCACTGATGTC
Db      773 TATGGGTCTGGAGGCTTTTGTCTATGCTTTCATTTAAATGATTCATCTCACTGATGTC
Qy      893 TCAGCACTGAGGCTGAGAGCTGTGCTGAGAG 926
Db      833 TGAAGAGCCCTAGCTTGAATAAGATTTTAAAGG 866
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## RESULT 3

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US-09-949-016-12790
; Sequence 12790, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CI.001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-628-464-1

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4313806 seqs, 287787103 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
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22: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	956.6	100.0	957	US-10-628-464-1	Sequence 1, Appl
2	249.8	26.1	924	US-09-825-882-17	Sequence 17, Appl
3	249.8	26.1	924	US-10-343-650A-679	Sequence 679, Appl
4	249.8	26.1	924	US-10-724-208-17	Sequence 17, Appl
5	249.8	26.1	924	US-10-770-127-188	Sequence 188, Appl
6	249.8	26.1	924	US-10-724-209-17	Sequence 17, Appl
7	249.8	26.1	1324	US-10-017-161-1785	Sequence 1785, Ap
8	249.8	26.1	1324	US-10-292-798-1441	Sequence 1441, Ap
9	214.8	22.4	3437	US-09-510-332-156	Sequence 156, App
10	214.8	22.4	3437	US-10-770-127-156	Sequence 156, App
11	192.4	20.1	1295	US-09-510-332-100	Sequence 100, App

12	192.4	20.1	1295	US-10-770-127-100	Sequence 100, App
13	118.8	12.4	341	US-09-510-332-159	Sequence 159, App
14	118.8	12.4	341	US-10-770-127-159	Sequence 159, App
15	112.2	11.7	2887	US-09-510-332-140	Sequence 140, App
16	112.2	11.7	2887	US-10-770-127-140	Sequence 140, App
17	111.6	11.7	876	US-09-393-634-65	Sequence 65, Appl
18	111.6	11.7	876	US-09-510-332-31	Sequence 31, Appl
19	111.6	11.7	876	US-10-383-982-65	Sequence 65, Appl
20	111.6	11.7	876	US-10-364-861-65	Sequence 65, Appl
21	111.6	11.7	876	US-10-770-127-31	Sequence 31, Appl
22	110.2	11.5	972	US-09-825-882-5	Sequence 5, Appl
23	110.2	11.5	972	US-10-343-650A-673	Sequence 673, App
24	110.2	11.5	972	US-10-724-208-5	Sequence 5, Appl
25	110.2	11.5	972	US-10-770-127-176	Sequence 176, Appl
26	110.2	11.5	972	US-10-724-209-5	Sequence 5, Appl
27	110.2	11.5	1372	US-10-017-161-2087	Sequence 2087, Ap
28	110.2	11.5	1372	US-10-017-161-2137	Sequence 2137, Ap
29	110.2	11.5	1372	US-10-292-798-1733	Sequence 1733, Ap
30	110.2	11.5	1372	US-10-292-798-1783	Sequence 1783, Ap
31	105.2	11.0	914	US-10-364-861-6	Sequence 6, Appl
32	105.2	11.0	1463	US-09-393-634-6	Sequence 6, Appl
33	105.2	11.0	1463	US-10-383-982-6	Sequence 6, Appl
34	105.2	11.0	6552	US-09-510-332-82	Sequence 82, Appl
35	105.2	11.0	6552	US-10-770-127-82	Sequence 82, Appl
36	96.8	10.1	1017	US-10-343-650A-677	Sequence 677, App
37	88.6	9.3	966	US-09-825-882-3	Sequence 3, Appl
38	88.6	9.3	966	US-10-724-208-3	Sequence 3, Appl
39	88.6	9.3	966	US-10-770-127-174	Sequence 174, App
40	88.6	9.3	966	US-10-724-209-3	Sequence 3, Appl
41	88.6	9.3	1017	US-10-343-650A-675	Sequence 675, App
42	88.6	9.3	1366	US-10-292-798-1731	Sequence 1731, Ap
43	88.6	9.3	1417	US-10-017-161-2085	Sequence 2085, Ap
44	88.6	9.3	1417	US-10-017-161-2139	Sequence 2139, Ap
45	88.6	9.3	1417	US-10-292-798-1785	Sequence 1785, Ap

#### ALIGNMENTS

RESULT 1  
US-10-628-464-1  
; Sequence 1, Application US/10628464  
; Publication No. US20040132134A1  
; GENERAL INFORMATION:  
; APPLICANT: ADIER, JON ELLIOT  
; APPLICANT: TANG, HUIXIAN  
; APPLICANT: PRONTIN, ALEXEY  
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
; FILE REFERENCE: 100317.54260US  
; CURRENT APPLICATION NUMBER: US/10/628,464  
; CURRENT FILING DATE: 2003-07-29  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 957  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(954)  
US-10-628-464-1

Query Match 100.0%; Score 956.6; DB 18; Length 957;  
Best Local Similarity 100.0%; Pred. No. 1.1e-299;  
Matches 957; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGAATGAGACACATGGTTCTAGATCTTCGATGCTGACAGAGGCCATCATCTTG 60  
QY 61 GTTACCATTTTACTCTTTTACGCTGTGATGACATGACAGGCAATGGCTTCATCATCTGCT 120  
DB 61 GTTACCATTTTACTCTTTTACGCTGTGATGACATGACAGGCAATGGCTTCATCATCTGCT 120

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QY 241 TTCTTGATCGAATGGGCTCCCATACACCTGATGAGTTCTAGCTTCCAGTGG 300
DB 241 TTCTTGATCGAATGGGCTCCCATACACCTGATGAGTTCTAGCTTCCAGTGG 300
QY 301 GACTTCTGATGCTGCGCACTTATGCTCTCACTGCTCACTGCTCTTATGTTG 360
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QY 361 AAAATTGCTACTTACCCACCTGCTTCTTCTGCTAAGCACAAGTTGCTGGGTG 420
DB 361 AAAATTGCTACTTACCCACCTGCTTCTTCTGCTAAGCACAAGTTGCTGGGTG 420
QY 421 CTACATGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 CTACATGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 ATAGGCAACCAAGAAATGATCAGAACTATTAAAGAACATCTACAACTTGAATGTC 540
DB 481 ATAGGCAACCAAGAAATGATCAGAACTATTAAAGAACATCTACAACTTGAATGTC 540
QY 541 ACTGGGATGCTATGAGGAGCTACTGTGAGAAATCTATCTTCTTCTTAAATGAT 600
DB 541 ACTGGGATGCTATGAGGAGCTACTGTGAGAAATCTATCTTCTTCTTAAATGAT 600
QY 601 ACTTGGCAATGCGCACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
DB 601 ACTTGGCAATGCGCACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
QY 661 GGAAGACACAGAAAGAGCTCTCTTCAACCTCAGAAATCCGAGAGCCAGTGTGAG 720
DB 661 GGAAGACACAGAAAGAGCTCTCTTCAACCTCAGAAATCCGAGAGCCAGTGTGAG 720
QY 721 GCAACATTAAGGCTGCTGCTGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
DB 721 GCAACATTAAGGCTGCTGCTGCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
QY 781 CTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 TGGAGTCACTGATTTATCTGTGTGAGAGTTCAACCCATCATCTGCTCTTCAAGAAC 900
DB 841 TGGAGTCACTGATTTATCTGTGTGAGAGTTCAACCCATCATCTGCTCTTCAAGAAC 900
QY 901 TGCAGGCTGAGAGCTGCTGCTGAGAGTGTCTTCTTCAAGGTGTGGAGACCTTGA 957
DB 901 TGCAGGCTGAGAGCTGCTGCTGAGAGTGTCTTCTTCAAGGTGTGGAGACCTTGA 957

RESULT 2
US-09-825-882-17
; Sequence 17, Application US/09825882
; Patent No. US20020094551A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-882-17

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Best Local Similarity 56.4%; Pred. No. 6.3e-70;
Matches 489; Conservative 0; Mismatches 372; Indels 6; Gaps 1;

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DB 21 CTCTCTGCTGCTGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 80
QY 114 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 173
DB 81 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140
QY 174 ATGCTTACCTAGAGGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 233
DB 141 CCGTATTAAGCTTGGGCTCTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 200
QY 234 TTATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 293
DB 201 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
QY 294 CCAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
DB 261 ACACTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 320
QY 354 TTGTGAAATTTGCTACCTTCAACCACTGCTCTTCTGCTGCTGCTGCTGCTGCT 413
DB 321 CTGTGGAAGATTTGCTAATCAACACACCTTCTGCTGCTGCTGCTGCTGCTGCT 380
QY 414 TGGGTGCTACCAATGAGCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
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QY 534 GATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 495 TGGGAACATGACCTAAGTGAATCAAGATTAAGAAATATTTCCATCCCTGAA 554
QY 594 AATGATTAATGGAACAATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
DB 555 ACTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
QY 654 ATCTGGAAGACACAGGAAGAGCTCTCTTCAACCTGAGATTCGAGAGCCGAG 713
DB 615 TTCTTGAAGAGCATACAGAAATGAGACACAGGCAAGCTGCAAGACCCGAG 674
QY 714 TGTGAGGACACATTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
DB 675 CACCAAGGCTCAACAGAGCTGTAAGTCCCTCATCTCTTCTCATTTAGCTGT 734
QY 774 ATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833
DB 834 CTGGGTGAGAGTCAATTTATCTGTGTGAGAGATTCACCCATCATCTGCTGCT 893
QY 795 CTGGCCATGGAATTTGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
DB 894 CAGCAACTGAGGCTGAGAGTGTGCT 920
855 CAGCAACCTCAAGCTTGAAGCTGTT 881
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RESULT 3

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 11:57:50 / Search time 3738 Seconds  
(without alignments)  
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Gapop 10.0, Gapext 1.0

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Post-processing: Minimum Match 0\*

Maximum Match 100\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	92	9.6	717	CF147792	CF147792 AGENCOURT
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3	69	7.2	787	A2739176	A2739176 RPECI-24-1
4	67.8	7.1	866	CN840760	CN840760 AGENCOURT
5	66.2	6.9	718	CF147794	CF147794 AGENCOURT
6	65	6.8	894	AY403664	AY403664 Mus muscu
7	64	6.7	804	CN841612	CN841612 AGENCOURT
8	63.4	6.6	493	B2898478	B2898478 CH240_14L
9	63	6.6	900	AY404526	AY404526 Homo sapi
10	62.4	6.5	917	CN842886	CN842886 AGENCOURT
11	62.4	6.5	707	CN843334	CN843334 AGENCOURT
12	62.4	6.5	863	CN843111	CN843111 AGENCOURT
13	62.4	6.5	885	CN843127	CN843127 AGENCOURT
14	62.2	6.5	771	CC544773	CC544773 CH240_427
15	61.8	6.5	900	AY404527	AY404527 Pan trogl
16	61.2	6.4	893	AY403663	AY403663 AGENCOURT
17	59.2	6.2	715	CF147795	CF147795 AGENCOURT
18	59	6.2	737	CO960534	CO960534 AGENCOURT
19	58	6.1	650	AQ316999	AQ316999 CITR1-E1-
20	58	6.1	742	AQ308694	AQ308694 CITR1-E1-
21	58	6.1	850	CN835406	CN835406 AGENCOURT
22	58	6.1	895	CN839536	CN839536 AGENCOURT
23	58	6.1	900	AY403662	AY403662 Homo sapi
24	57.6	6.0	744	CO935442	CO935442 AGENCOURT

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C	26	56.8	5.9	790	7	CO959975	CO959975 AGENCOURT
C	27	56.2	5.9	894	9	AY404528	AY404528 Mus muscu
C	28	55.6	5.8	2418	3	AF116728	AF116728 Homo sapi
C	29	54.4	5.7	397	8	AQ164951	AQ164951 HS_3014_B
C	30	53.8	5.6	530	9	CE673154	CE673154 tigr-gss-
C	31	53.6	5.6	414	4	BH614820	BH614820 UP_535-10
C	32	53.6	5.6	806	4	BG209561	BG209561 RST29087
C	33	53.6	5.6	884	7	CN839562	CN839562 AGENCOURT
C	34	53.2	5.6	851	9	CC521365	CC521365 CH240_369
C	35	52.2	5.5	689	7	CO959518	CO959518 AGENCOURT
C	36	52	5.4	921	7	CN843110	CN843110 AGENCOURT
C	37	51.8	5.4	330	2	AW266498	AW266498 ZC24_gast
C	38	51.8	5.4	758	4	BG203110	BG203110 RST2479
C	39	51.4	5.4	498	8	AO616191	AO616191 HS_5148_A
C	40	51.2	5.4	681	9	CE066229	CE066229 tigr-gss-
C	41	50.8	5.3	639	8	B2922748	B2922748 CH240_115
C	42	50.2	5.2	466	8	B17827	B17827 3471.9_TPB
C	43	48.8	5.1	852	7	CN835976	CN835976 AGENCOURT
C	44	47.4	5.0	776	8	B2842365	B2842365 CH240_239
C	45	45.8	4.8	921	7	CN835918	CN835918 AGENCOURT

#### ALIGNMENTS

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LOCUS  
DEFINITION  
AGENCOURT 14740222 NIH MGC 145 Homo sapiens cDNA clone  
IMAGE:6971939 5', mRNA sequence.  
VERSION  
CF147792  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 717)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-x@mail.nih.gov](mailto:cgabs-x@mail.nih.gov)  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: IRB102 row e column: 10  
High quality sequence stop: 713.  
Location/Qualifiers

#### FEATURES

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/clone="IMAGE:6971939"  
/issue\_type="mixed"  
/lab\_host="DH10B"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XhoI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1\\_presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1_presv.dat)





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 14:27:28 ; Search time 4374 Seconds  
(without alignments)  
10601.656 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 957

Sequence: 1 atgaatggagacacatggt.....caagtggtggacacttga 957

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl: 1: gb\_ba: 2: gb\_hgt: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pat: 7: gb\_ph: 8: gb\_pl: 9: gb\_dr: 10: gb\_ro: 11: gb\_sts: 12: gb\_sy: 13: gb\_un: 14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	957	AY724955	AY724955 Homo sapi
2	929	97.1	954	BD171274	BD171274 Novel G p
3	929	97.1	954	BD185566	BD185566 Novel G p
4	929	97.1	957	CQ738424	CQ738424 Sequence
5	929	97.1	957	CQ800046	CQ800046 Sequence
6	929	97.1	957	AY114094	AY114094 Homo sapi
7	929	97.1	72045	AC092214	AC092214 Homo sapi
8	437	45.7	957	AY724901	AY724901 Pan trogl
9	419	43.8	957	AY724866	AY724866 Pan panis
10	176	18.4	957	AY724923	AY724923 Gorilla g
11	114	11.9	957	AY724986	AY724986 Pongo pyg
12	81	8.5	957	AY725022	AY725022 Macaca mu
13	47	4.9	131565	AC143122	AC143122 Macaca mu
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15	26	2.7	26	BD185571	BD185571 Novel G p
16	26	2.7	32	BD171275	BD171275 Novel G p
17	26	2.7	32	BD185567	BD185567 Novel G p
18	25	2.6	32	BD171276	BD171276 Novel G p
19	25	2.6	32	BD185568	BD185568 Novel G p

20	23	2.4	6	BD171277	BD171277 Novel G p
21	23	2.4	6	BD185569	BD185569 Novel G p
22	23	2.4	224803	AC111351	AC111351 Rattus no
23	23	2.4	252616	AC122593	AC122593 Rattus no
24	22	2.3	22	BD171278	BD171278 Novel G p
25	22	2.3	22	BD185570	BD185570 Novel G p
26	22	2.3	966	AY362748	AY362748 Rattus no
27	22	2.3	966	AF532786	AF532786 Mus muscu
28	22	2.3	111375	AC073878	AC073878 Homo sapi
29	22	2.3	203639	AC117625	AC117625 Mus muscu
30	22	2.3	216647	CNS05TCO	AL355773 Human chr
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## ALIGNMENTS

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LOCUS Homo sapiens chromosome 7 taste receptor T2R56 gene, complete cds.  
DEFINITION AY724955  
ACCESSION AY724955.1 GI:51989208  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

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DEFINITION Novel G protein-coupled receptor protein and DNA thereof.  
ACCESSION BD171274  
VERSION BD171274.1 GI:27877086

KEYWORDS WO 02057309-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 954)  
AUTHORS Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.  
TITLE Novel G protein-coupled receptor protein and DNA thereof  
JOURNAL Patent: WO 02057309-A 1 25-JUL-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD,MASANORI MIWA,TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA  
COMMENT OS Homo sapiens (human)  
EN WO 02057309-A/1  
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PF 17-JAN-2002 WO 2002JP000271  
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LOCUS	
DEFINITION	BD185566 954 bp DNA linear PAT 17-JUN-2003
ACCESSION	BD185566
VERSION	BD185566.1 GI:31877766
KEYWORDS	JP 2002360279-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 954)
TITLE	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.
JOURNAL	Novel G protein-coupled receptor and its DNA Patent: JP 2002360279-A 1 17-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD OS Homo sapiens (human) PN JP 2002360279-A/1 PD 17-DEC-2002 PI 17-JAN-2002 JP 2002008445 PT MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC C12N5/09, A61K39/395, A61K45/00, A61P1/00, A61P3/00, PC A61P9/00 PC A61P9/00, A61P11/00, A61P25/28, A61P29/00, A61P31/00, A61P35/00, PC A61P37/00, PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC C12P21/02. PC C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/53, PC G01N33/56, PC C12N5/00, C12N5/00 CC Novel G protein-coupled receptor and its DNA FH Location/Qualifiers FT source 1..954 /organism='Homo sapiens (human)'. 1..954 Location/Qualifiers

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VERSION CQ738424.1 GI:42339256  
KEYWORDS  
SOURCE  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
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Patent: WO 0206879-A 24358 06-SEP-2002;  
JOURNAL PE Corporation (NY) (US)  
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SEQUENCE 50 from Patent WO2004029087.  
DEFINITION  
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ACCESSION  
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REFERENCE  
AUTHORS Bufe, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.  
TITLE Bitter taste receptors  
JOURNAL Patent: WO 2004029087-A 50 08-APR-2004;  
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DEFINITION Homo sapiens putative taste receptor T2R60 gene, complete cds.  
ACCESSION AY114094  
VERSION AY114094.1 GI:28603637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 957) Mammalia; Euteleostomi; Primates; Carnivora; Hominoidea; Homo.  
TITLE Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
Identification and characterization of human taste receptor genes  
belonging to the TAS2R family  
JOURNAL Cytogenet. Genome Res. 98 (1), 45-53 (2002)  
MEDLINE 12584440  
PUBMED 22471936  
REFERENCE  
AUTHORS Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
TITLE Direct Submission  
JOURNAL Submitted (17-May-2002) Pharma Research Basel, F. Hoffmann-La Roche  
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Qy 901 TGCAGGCTGAGAGCTGTGCTGAAGATGCTG 929  
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RESULT 7  
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LOCUS  
DEFINITION  
AC092214  
VERSION  
AC092214.3  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AC092214 72045 bp DNA linear PRI 31-JAN-2004  
Homo sapiens BAC clone RP11-81109 from 7, complete sequence.  
AC092214.3 GI:16931065  
HTG.

REFERENCE  
AUTHORS  
1 (bases 1 to 72045)  
Hillier, L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Wylie, K., Sekhon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delaney, K.D., Miner, T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Bradshaw-Cordum, H., All, J., Andrews, S., Isak, A., Vanbrunt, A., Nguyen, C., Du, F., Lamar, B., Courtney, L., Kallick, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Hartings, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowski-Reilly, A., Leonard, S., Kohlfing, T., Rock, S.M., Tin-Mollam, A.M., Abbott, A., Minx, P., Maupin, R., Stromwater, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Moesamer, J.P., Wendt, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W., Spiekh, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Mardis, E.R., Clifton, S.W., Chissole, S.L., Marra, M.A., Raymond, C., Haugen, E., Gillet, M., Zhou, Y., James, R., Phelps, K., Iadonoto, S., Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Furey, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Fliscek, P., Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Tortorelli, D., Chinai, A.A., T. Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Eichler, E., Green, E.D., Waterston, R.H. and Wilson, R.K.  
The DNA sequence of human chromosome 7  
Nature 424 (6945), 157-164 (2003)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
12853948  
2 (bases 1 to 72045)  
Doebber, A., Elliott, G., Kozlowski, A. and Sun, H.  
The sequence of Homo sapiens BAC clone RP11-81109  
Unpublished (2001)  
3 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (29-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
4 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (15-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
5 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
6 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (10-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
7 (bases 1 to 72045)  
Wilson, R.  
Direct Submission  
Submitted (31-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Nov 15, 2001 this sequence version replaced gi:15625026.

COMMENT

----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [sapiens@wustl.edu](mailto:sapiens@wustl.edu)  
----- Summary Statistics  
Center project name: H\_NH081109  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send [mailto:egreen@nhgri.nih.gov](mailto:mailto:egreen@nhgri.nih.gov), or see <http://genome.wustl.edu>

SOURCE INFORMATION:  
The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Caranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-563K23 the clone sequenced to the right is RP11-298A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-81109 actual end is at base position 140619 of RP11-298A10.

#### FEATURES

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RESULT 8

AY724901

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

957 bp DNA linear PRI 18-SEP-2004

chromosome 7 taste receptor T2R56 gene, complete

AY724901 GI:51989117

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

1 (bases 1 to 957)

Anne F., Yoav G., Orna M. and Svante P.

Evolution of bitter taste receptors in human and apes

Unpublished

2 (bases 1 to 957)

AUTHORS Anne, F., Yeav, G., Orna, M. and Svante, P.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

## FEATURES

source

Location/Qualifiers

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CDS

## ORIGIN

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Qy 874 CACCCCATATCTGCTCTTCAAGCACTGACAGCTGAGAGCTGTGCTGAAGCTG 929

Db 874 CACCCCATATCTGCTCTTCAAGCACTGACAGCTGAGAGCTGTGCTGAAGCTG 929

RESULT 9  
AY724866 957 bp DNA linear PRI 18-SEP-2004

LOCUS Pan paniscus chromosome 7 taste receptor T2R56 gene, complete cds.

DEFINITION AY724866

ACCESSION AY724866

VERSION AY724866.1 GI:51989057

KEYWORDS

SOURCE Pan paniscus (pygmy chimpanzee)

ORGANISM Pan paniscus

REFERENCE 1 (bases 1 to 957)

AUTHORS Anne, F., Yeav, G., Orna, M. and Svante, P.

TITLE Evolution of bitter taste receptors in human and apes

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 957)

AUTHORS Anne, F., Yeav, G., Orna, M. and Svante, P.

TITLE Direct Submission

JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for

Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,

Germany

FEATURES

source

Location/Qualifiers

1..957

/organism="Pan paniscus"

/mol\_type="genomic DNA"

/db\_xref="taxon:9597"

/chromosome="7"

1..957

/codon\_start=1

/product="taste receptor T2R56"

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EVLRLMLPCDKLIVSLASHFCLQSVWGKTIYFLPMAPNPVLOFLAFQDF  
LNAATLWFSTLWLVYCVKIAITPTHPVFMKRLSGMLPMWFSVGLSPTLLIF  
IGNHMYONVYLKNHLOPMNVNTGNSIRSYCEKFLPLKMTITWTPAVFPICMILLIT  
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KFWMESVIYLCAAVHPILLFNSCRRLRAVLKRSRSRCGTP"

ORIGIN

Query Match 43.8%; Score 419; DB 9; Length 957;

Best Local Similarity 98.9%; Pred. No. 6.4e-225;

Matches 919; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ATGAATGAGACCAATGTTCTAGATCTTGGTGAAGTGAAGAGCCATCATCTTG 60

Db 1 ATGAATGAGACCAATGTTCTAGATCTTGGTGAAGTGAAGAGCCATCATCTTG 60

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Db 61 GTTACATTTTACTCTTTTAAAGCTGTGTAAGCAATGAGGCAATGGCTTCACTGCT 120

Qy 121 GCTCTGGGCGTGAAGTGTGCTACGAGAAATGTTGCTTGTGATAAGTTATTTGTT 180

Db 121 GCTCTGGGCGTGAAGTGTGCTACGAGAAATGTTGCTTGTGATAAGTTATTTGTT 180

Qy 181 AGCTTAAGGAGGCTCTGCTTCTGCTGAGTCAAGTGAATGGTAAGCACTTAATGTT 240

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 13:25:01 ; Search time 622 Seconds  
(without alignments)  
9108.026 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	929	97.1	954	6	ABK87584 DNA encod
2	929	97.1	957	12	ADJ87104 Nucleotid
3	929	97.1	957	13	ADM33336 Adm33336 Human bit
4	26	2.7	26	6	ABK87589 Novel hum
5	26	2.7	32	6	ABK87585 Novel hum
6	25	2.6	32	6	ABK87586 Novel hum
7	23	2.4	23	6	ABK87587 Novel hum
8	22	2.3	22	6	ABK87588 Novel hum
9	22	2.3	939	8	ACC44449 Gene enco
10	21	2.2	433	6	ABN24775 Human ORF
11	21	2.2	954	10	ADBO7626 Novel cod
12	20	2.1	686	6	ABQ65740 Arabidops
13	20	2.1	879	3	AAC40611 Arabidops
14	20	2.1	1235	3	AAZ52509 Human sec
15	20	2.1	13308	6	AAK98531 Human eno
16	19	2.0	248	4	AAI56241 Probe #24
17	19	2.0	248	4	AAK24246 Human bra
18	19	2.0	248	4	ABSA4918 Human liv
19	19	2.0	248	6	ABS23758 Human gen
20	19	2.0	263	4	AAI22458 Probe #12

C	21	19	2.0	263	4	ABA67533 Human foe
C	22	19	2.0	263	4	AAI47750 Probe #16
C	23	19	2.0	263	4	ABA49632 Human bre
C	24	19	2.0	263	4	ABA34615 Probe #13
C	25	19	2.0	263	4	AAK41705 Human bon
C	26	19	2.0	263	4	AAK15959 Human bra
C	27	19	2.0	263	4	ABSA41294 Human liv
C	28	19	2.0	263	5	AAI08145 Human #81
C	29	19	2.0	263	6	ABS15711 Human gen
C	30	19	2.0	387	4	AAI13223 Probe #31
C	31	19	2.0	387	4	ABA54921 Human foe
C	32	19	2.0	387	4	AAI34576 Probe #32
C	33	19	2.0	387	4	ABA44481 Human bre
C	34	19	2.0	387	4	ABA24690 Probe #31
C	35	19	2.0	387	4	AAK28650 Human bon
C	36	19	2.0	387	4	AAK03196 Human bra
C	37	19	2.0	387	4	ABS28246 Human liv
C	38	19	2.0	387	5	AAI03129 Probe #31
C	39	19	2.0	387	6	ABS03158 Human gen
C	40	19	2.0	485	4	AAI10206 Probe #13
C	41	19	2.0	485	4	ABA51843 Human foe
C	42	19	2.0	485	4	AAI31458 Probe #14
C	43	19	2.0	485	4	ABA21670 Probe #13
C	44	19	2.0	485	4	AAK25586 Human bon
C	45	19	2.0	485	4	AAK00146 Human bra

#### ALIGNMENTS

RESULT 1	ABK87584	standard; cDNA; 954 BP.
ID	ABK87584	standard; cDNA; 954 BP.
AC	ABK87584;	
DT	24-SEP-2002	(first entry)
XX		
DE	DNA encoding novel human G-protein coupled receptor.	
XX		
KW	G-protein coupled; receptor; liver; central nervous system disease;	
KW	Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;	
KW	hyperlipemia; cancer; non-small cell lung cancer; ovarian cancer;	
KW	stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;	
KW	circulatory disease; hypertension; atherosclerosis; angina; allergy;	
KW	inflammatory disease; respiratory disease; asthma; bronchitis;	
KW	digestive disease; stomach ulcer; duodenal ulcer; immune disorder;	
KW	autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;	
KW	pneumonia; influenza; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..954
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FT		/product= "Novel G-protein coupled receptor"
FT		/partial
FT		/note= "No stop codon given"
XX		
XX	WO200257309-A1.	
XX	25-JUL-2002.	
XX	17-JAN-2002; 2002WO-JP000271.	
XX	18-JAN-2001; 2001JP-00010814.	
XX	30-MAR-2001; 2001JP-00102558.	
XX	(TAKE ) TAKEDA CHEM IND LTD.	
XX	MIWA M, Ito T, Shintani Y, Miyajima N,	
XX	WPI; 2002-538457/57.	

DR P-PSDB; AAU98514.  
 XX New G-protein coupled receptor protein expressed in human liver for  
 PT design of drugs and reagents for treatment and diagnosis of cancer and  
 PT respiratory metabolic and other diseases.  
 XX  
 PS Claim 6, Page 91; 101pp; Japanese.  
 XX  
 CC The invention describes a novel G-protein coupled receptor protein  
 CC expressed in human liver. The protein is used in the treatment,  
 CC prevention and diagnosis of central nervous system diseases (such as  
 CC Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes  
 CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
 CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
 CC circulatory diseases (such as hypertension, atherosclerosis and angina),  
 CC inflammatory diseases (such as allergy and rheumatism), respiratory  
 CC diseases (such as asthma and bronchitis), digestive diseases (such as  
 CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
 CC diseases), and infections (such as acquired immunodeficiency syndrome  
 CC (AIDS), pneumonia and influenza). This sequence encodes the novel G-  
 CC protein coupled receptor protein described in the invention  
 XX  
 XX  
 SQ Sequence 954 BP; 202 A; 241 C; 214 G; 297 T; 0 U; 0 Other;  
 Query Match 97.1%; Score 929; DB 6; Length 954;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAATGGAGACACAGATGGTTCTAGAGATTCCTGGTACTGACAGAAAGGCCATCATCTTG 60  
 DB 1 ATGAATGGAGACACAGATGGTTCTAGAGATTCCTGGTACTGACAGAAAGGCCATCATCTTG 60  
 QY 61 GTTACCATTTTACTCTTTTACGCTGTGTAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
 DB 61 GTTACCATTTTACTCTTTTACGCTGTGTAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
 QY 121 GCTCTGGGCGCTGGAGTGGGTGTCTACGAGAAATGTTGCTGCTGTGATTAATTTGGTT 180  
 DB 121 GCTCTGGGCGCTGGAGTGGGTGTCTACGAGAAATGTTGCTGCTGTGATTAATTTGGTT 180  
 QY 181 AGCCTAGGGGCGCTGGCTCTGTGTGCACTGAGTGTATGGGTAAAGACATTTATGTT 240  
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 DB 481 ATAGGCAACCAAGATGTATCAAGAACTATTAAAGAACCATTTACAACCTTGGAAATGC 540  
 QY 541 ACTGGGATAGCAATAGGAGCTACTGTGAGAAATTTCAATCTTCCCTCTAAAGAAATGAT 600  
 DB 541 ACTGGGATAGCAATAGGAGCTACTGTGAGAAATTTCAATCTTCCCTCTAAAGAAATGAT 600  
 QY 601 ACTTGGACATGCGCACTGCTCTTTTCAATTTGATTTGCTCATCATCATCTG 660  
 DB 601 ACTTGGACATGCGCACTGCTCTTTTCAATTTGATTTGCTCATCATCATCTG 660  
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DB 661 GGAAGACACAGAAAGAGCTTCTCTTAAACCTCAGGATTCGAGAGCCCAAGTGTGACG 720  
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 DB 721 GCACACATAAAGAGCTGTGCTGCTCTCTCTCTTTTGCCATGCTCTTCAATCATATTTC 780  
 QY 781 CTGTCACTGGTGTTCAGTGTGCTGCTGAGTATTTTCCACTGTGACTTTAAATTTGGGTG 840  
 DB 781 CTGTCACTGGTGTTCAGTGTGCTGCTGAGTATTTTCCACTGTGACTTTAAATTTGGGTG 840  
 QY 841 TGGGAGTCACTGATTTATCTGTGTGAGAGATTACCCCATATTTGCTCTTACAGAAC 900  
 DB 841 TGGGAGTCACTGATTTATCTGTGTGAGAGATTACCCCATATTTGCTCTTACAGAAC 900  
 QY 901 TGCAGGCTAGAGCTGTGCTGTAAGAGTGC 929  
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## RESULT 2

ADJ87104 standard; DNA; 957 BP.

ADJ87104;

06-MAY-2004 (first entry)

Nucleotide sequence of human bitter taste receptor T2R76.

Human; bitter taste receptor ; T2R76; chromosome 7; bitter taste ; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..957 /tag= a /product= "bitter taste receptor T2R76"

PN MO2004011617-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023604.

PR 29-JUL-2002; 2002US-0398727P.

PA (SENO-) SENOMYX INC.

PA (ADLE/) ADLER J E.

PA (TANG/) TANG H.

PA (PRON/) PRONIN A.

PA (ZOLL/) ZOLLER M.

PI Adler JE, Tang H, Pronin A, Zoller M;

DR MPI; 2004-143845/14.

P-PSDB; ADJ87105.

PT Novel isolated bitter taste receptor, T2R76 polypeptide useful for

XX identifying modulators of taste perception, or bitter compounds.

XX Claim 1; Page 97-98; 100pp; English.

XX The present sequence encodes human bitter taste receptor T2R76. The human

XX T2R76 gene is located on chromosome 7 in the region 144062692-144063648.

XX The reading frame of T2R76 is intronless. T2R76 polypeptides and

XX CC polynucleotides are useful for identifying modulators. Such modulators

XX CC are useful for modulating bitter taste perception in a subject. T2R76

XX CC agonists can be administered to enhance bitter tastes, while T2R76

XX CC antagonists can be administered to reduce bitter taste.

XX Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;

Query Match 97.1%; Score 929; DB 12; Length 957;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 TTCTTGATCCGATGGCTTCCATACACCTGTATGCAATTTTACCTTTTCAAGTGG 300

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DB 361 AAAATGCTACCTTACCCACCTGCTGCTTCTTGTGGTAAAGCAAGTGTGGTGG 420

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DB 541 ACTGGCGATGACATACGAGAGCTACTGTAGAAATTTATCTTCCCTTAAAAATGAT 600

QY 601 ACTTGGCAATGCCCACTGCTGCTTTTTCATTTGCAATGTTTGTCTATCATCTCTG 660  
DB 601 ACTTGGCAATGCCCACTGCTGCTTTTTCATTTGCAATGTTTGTCTATCATCTCTG 660

QY 661 GGAAGACAGAGAAAGGCTCTCTTCAACACTCAGGATTCGAGAGCCAGTGTGAG 720  
DB 661 GGAAGACAGAGAAAGGCTCTCTTCAACACTCAGGATTCGAGAGCCAGTGTGAG 720

QY 721 GCAACATAAAGGCTCTGCTGCTCTCTCTCTTTTGCATGCTTTCATCTCATATTT 780  
DB 721 GCAACATAAAGGCTCTGCTGCTCTCTCTCTTTTGCATGCTTTCATCTCATATTT 780

QY 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 TGGAGTCAGATGATTTATCTGTGTGAGAGAGTTACCCCATCATTTCTTTCAGCAAC 900  
DB 841 TGGAGTCAGATGATTTATCTGTGTGAGAGAGTTACCCCATCATTTCTTTCAGCAAC 900

QY 901 TGCAGGCTGAGAGCTGTGCTGAGAGTGC 929  
DB 901 TGCAGGCTGAGAGCTGTGCTGAGAGTGC 929

RESULT 3  
ADM3336  
ID ADM3336 standard; cDNA; 957 BP.  
XX

AC ADM33336;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.  
XX  
KM human; bitter taste receptor; food; gene; ss.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT 1.957  
FT CDS /\*tag= a  
FT /product= "bitter taste receptor hTAS2R60"  
FN NC02004029087-A2.  
XX  
PD 08-APR-2004.  
XX  
PE 25-SEP-2003; 2003MO-EP010691.  
PF 25-SEP-2002; 2002US-0413298P.  
PR 25-SEP-2002; 2002US-0413298P.  
XX  
PA (DEBR-) DEUT INST ERNAERUNGSPOTSDAM.  
PI Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
XX WPI; 2004-305149/28.  
DR P-PSDB; ADM33335.  
XX  
PT Novel bitter receptor polynucleotide encoding human TAS2R protein having  
PT bitter substance binding activity, useful for producing nutraceutical or  
PT pharmaceutical compositions comprising antagonists of bitter taste  
PT receptor activity.  
XX  
PS Claim 14; SEQ ID NO 50; 108bp; English.  
XX  
CC The present sequence encodes a human bitter taste receptor. Also  
CC described: (1) a polynucleotide encoding a bitter taste receptor (1); (2)  
CC a vector (II) containing (1); (3) a host cell (III) genetically  
CC engineered with (1) or (II); (4) a transgenic non-human animal (IV)  
CC containing (1), (II) and/or (III); (5) a polypeptide (V) having the amino  
CC acid sequence encoded by (1) or obtained by culturing (III) and  
CC recovering polypeptide; (6) an antibody (VII) specifically binding to (V);  
CC (7) a nucleic acid molecule (VII) specifically hybridizing to (1); (8) an  
CC antagonist/inhibitor (VII) against (V) which is antibody, the  
CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
CC isolating (M1) an antagonist that binds to (V) encoded by (1); (10)  
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
CC foodstuff including human and animal foodstuff, any precursor material or  
CC additive employed in the production of foodstuff comprising (VII); and  
CC (12) a nutraceutical/pharmaceutical composition comprising (VII); and an  
CC active agent and optionally a carrier. (III) is useful for producing a  
CC polypeptide encoded by (1), which involves culturing (III) and recovering  
CC the polypeptide encoded by (1). (II) is useful for producing cells  
CC capable of expressing at least one of the bitter taste receptor  
CC polypeptide, which involves genetically cells in vitro with (II), where  
CC the bitter taste receptor polypeptide(s) is/are encoded by (1). (M1) or  
CC (M2) can be used for producing food or any precursor material or additive  
CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
CC for producing nutraceutical or pharmaceutical compositions. (1), (II),  
CC (VI) or (VIII) can be used for manufacturing a medicament for the  
CC treatment of an abnormally increased or decreased sensitivity towards a  
CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminated bitter tasting components of food and effectively useful in  
CC food industries.  
XX  
SQ Sequence 957 BP; 203 A; 240 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 97.1%; Score 929; DB 13; Length 957;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAATGAGACCATGATGTTCTTACGATCTTCGGTACAGACAGAGGCCATCATCTTG 60
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DB 61 GTTACCAATTTTACTCTCTTTTACGCTTGTGTGCAATAGCAGGCAATGGCTTCACTACTGCT 120
QY 121 GCTCTGGAGCGTGGAGTGGTGTCTACGAGAAATGTTGTGCTTGTGTATTAATGTT 180
DB 121 GCTCTGGAGCGTGGAGTGGTGTCTACGAGAAATGTTGTGCTTGTGTATTAATGTT 180
QY 181 AGCCTTAGGGGCTCTGCTCTCTGTCTGACAGTGTGTAATGGGTAAGACCATTTATGTT 240
DB 181 AGCCTTAGGGGCTCTGCTCTCTGTCTGACAGTGTGTAATGGGTAAGACCATTTATGTT 240
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DB 241 TTCTTGATTCGATTCGATTCGCTTCCCATACACCTGTACTGAGATTTCTAGTTTCCAGTGG 300
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DB 301 GACTTCTGTAATGCTGCGACCTTATGATGCTCTTACCTGCTCAGTGTCTTCTTATGTTG 360
QY 361 AAAATTGCTACCTTCAACCCACCTGTCTTCTGCTTAAAGACAAGTTGTCTGGGTGG 420
DB 361 AAAATTGCTACCTTCAACCCACCTGTCTTCTGCTTAAAGACAAGTTGTCTGGGTGG 420
QY 421 CTACCATGATGCTCTTCACTCTGTAGGGCTCTCCAGCTTCAACCATTTCTATTTTTC 480
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QY 481 ATAGGCAACCAAGAAATGATACAACTATTTTAAAGAAACATGTACAACTTGGAAATGTC 540
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DB 721 GCACACATAAAGGCTGTGCTGCTCTCTCTTTTGGCAATGCTTTGATTCGATATTTTC 780
QY 781 CTGTCACTGTGTCTTCACTGTGTGAGGATTTTTCACCTTGAACCTTTAAATCTGGGTG 840
DB 781 CTGTCACTGTGTCTTCACTGTGTGAGGATTTTTCACCTTGAACCTTTAAATCTGGGTG 840
QY 841 TGGAGAGTCACTGATTTATCTGTGTGAGAGTTCACCCCATCATCTTGTCTTCAAGAAC 900
DB 841 TGGAGAGTCACTGATTTATCTGTGTGAGAGTTCACCCCATCATCTTGTCTTCAAGAAC 900
QY 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGC 929
DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGC 929
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RESULT 4  
ABK87589  
ID ABK87589 standard; DNA: 26 BP.  
XX  
AC ABK87589;  
XX  
DT 24-SEP-2002 (first entry)  
XX

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DE Novel human G-protein coupled receptor related probe.
XX
XX G-protein coupled; receptor; liver; central nervous system disease;
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;
XX hyperlipaemia; cancer; non-small cell lung cancer; ovarian cancer;
XX stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;
XX circulatory disease; hypertension; atherosclerosis; angina; allergy;
XX inflammatory disease; respiratory disease; asthma; bronchitis;
XX digestive disease; stomach ulcer; duodenal ulcer; immune disorder;
XX autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;
XX pneumonia; influenza; probe; ss.
XX
XX Homo sapiens.
XX
XX PN MO200257309-A1.
XX
XX 25-JUL-2002.
XX
XX 17-JAN-2002; 2002MO-JP000271.
XX
XX 18-JAN-2001; 2001JP-00010814.
XX 30-MAR-2001; 2001JP-00102558.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Miwa M, Ito T, Shintani Y, Miyajima N;
XX WPI; 2002-538457/57.
XX
XX New G-protein coupled receptor protein expressed in human liver for
XX PT design of drugs and reagents for treatment and diagnosis of cancer and
XX PT respiratory metabolic and other diseases.
XX
XX Example 2; Page 93; 101pp; Japanese.
XX
XX The invention describes a novel G-protein coupled receptor protein
XX CC expressed in human liver. The protein is used in the treatment,
XX CC Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes
XX CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian
XX CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),
XX CC circulatory diseases (such as hypertension, atherosclerosis and angina),
XX CC inflammatory diseases (such as allergy and rheumatism), respiratory
XX CC diseases (such as asthma and bronchitis), digestive diseases (such as
XX CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune
XX CC disease), and infections (such as acquired immunodeficiency syndrome
XX CC (AIDS), pneumonia and influenza). This sequence represents a probe used
XX CC in the study of the novel G-protein coupled receptor protein described in
XX CC the invention
XX
XX Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 26; DB 6; Length 26;
XX Best Local Similarity 100.0%; Pred.No. 0.036;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 716 TGCAGGACACATPAAAGGCTGTGCTG 741
DB 1 TGCAGGACACATPAAAGGCTGTGCTG 26
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RESULT 5  
ABK87585  
ID ABK87585 standard; DNA: 32 BP.  
XX  
AC ABK87585;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Novel human G-protein coupled receptor, PCR primer #1.  
XX  
XX G-protein coupled; receptor; liver; central nervous system disease;  
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;  
XX



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:48:11 : Search time 207 Seconds

(without alignments)  
7564.816 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 957  
Sequence: 1 atgaatgagagaccacatgtg.....caagtgctgagacacttga 957

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2.1	1235	4	US-09-311-021-69	Sequence 69, Appl
2	2.1	62311	4	US-09-949-016-14582	Sequence 14582, A
3	2.0	4059	4	US-09-774-528-316	Sequence 316, App
4	2.0	42373	4	US-09-949-016-16348	Sequence 16348, A
5	2.0	73519	4	US-09-949-016-16344	Sequence 16344, A
6	2.0	98567	4	US-09-949-016-11750	Sequence 11750, A
7	2.0	105919	4	US-09-949-016-11769	Sequence 11769, A
8	1.9	290	4	US-09-513-999C-153	Sequence 153, App
9	1.9	372	4	US-09-248-796A-4118	Sequence 4118, Ap
10	1.9	381	4	US-09-270-767-14634	Sequence 14634, A
11	1.9	410	4	US-09-513-999C-3046	Sequence 3046, Ap
12	1.9	507	4	US-09-949-016-3571	Sequence 3571, Ap
13	1.9	601	4	US-09-949-016-53362	Sequence 53362, A
14	1.9	601	4	US-09-949-016-93241	Sequence 93241, A
15	1.9	601	4	US-09-949-016-130397	Sequence 130397, A
16	1.9	601	4	US-09-949-016-186249	Sequence 186249, A
17	1.9	601	4	US-09-949-016-186250	Sequence 186250, A
18	1.9	601	4	US-09-949-016-186251	Sequence 186251, A
19	1.9	663	4	US-09-975-327A-3	Sequence 3, Appl
20	1.9	722	3	US-08-998-416-331	Sequence 631, App
21	1.9	820	4	US-09-799-451-742	Sequence 742, App
22	1.9	865	4	US-09-949-016-4339	Sequence 4339, App
23	1.9	892	3	US-08-968-768B-1	Sequence 1, Appl
24	1.9	1891	4	US-09-949-016-1947	Sequence 1947, App
25	1.9	2540	4	US-09-799-451-463	Sequence 463, App
26	1.9	5099	3	US-09-610-040-5	Sequence 5, Appl
27	1.9	5099	4	US-10-267-763-5	Sequence 5, Appl

28	1.9	6759	4	US-09-949-016-13689	Sequence 13689, A
29	1.9	7571	4	US-09-949-016-15313	Sequence 15313, A
30	1.9	52661	4	US-09-949-016-17191	Sequence 17191, A
31	1.9	55226	4	US-09-949-016-14426	Sequence 14426, A
32	1.9	56694	4	US-09-949-016-15423	Sequence 15423, A
33	1.9	56702	4	US-09-949-016-15423	Sequence 15423, A
34	1.9	63644	4	US-09-949-016-12098	Sequence 12098, A
35	1.9	112239	4	US-09-949-016-13144	Sequence 13144, A
36	1.9	136088	4	US-09-949-016-12565	Sequence 12565, A
37	1.9	136480	4	US-09-949-016-17064	Sequence 17064, A
38	1.9	139936	4	US-09-949-016-11782	Sequence 11782, A
39	1.9	139952	4	US-09-949-016-13280	Sequence 13280, A
40	1.9	161652	4	US-09-497-855A-40	Sequence 40, Appl
41	1.9	200663	4	US-09-949-016-12569	Sequence 12569, A
42	1.9	278866	4	US-09-949-016-13922	Sequence 13922, A
43	1.9	278866	4	US-09-949-016-13923	Sequence 13923, A
44	1.9	278866	4	US-09-949-016-13924	Sequence 13924, A
45	1.9	278866	4	US-09-949-016-13925	Sequence 13925, A

#### ALIGNMENTS

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US-09-311-021-69
; Sequence 69, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 1235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-69

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Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      412  GGCTCTGCTGCTCTCTCT 431

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; Sequence 14582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J., Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 14582
; LENGTH: 62311
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62311)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14582
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Best Local Similarity 2.1%; Score 20; DB 4; Length 62311;
Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2244 GGAGTGGTCTACGAGAA 2225
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## RESULT 3

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US-09-774-528-316
; Sequence 316, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Aundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 316
; LENGTH: 4059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(3131)
US-09-774-528-316
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Best Local Similarity 2.0%; Score 19; DB 4; Length 4059;
Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 450 GCTCTCAGCTTACACACC 468
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US-09-949-016-16438/C
; Sequence 16438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16438
; LENGTH: 42373
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(42373)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16438
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Best Local Similarity 2.0%; Score 19; DB 4; Length 42373;
Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## RESULT 5

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; Sequence 16344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16344
; LENGTH: 73519
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(73519)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16344
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Query Match
Best Local Similarity 2.0%; Score 19; DB 4; Length 73519;
Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 582 CTTCCCTTAAATGATT 600
Db 53035 CTTCCCTTAAATGATT 53053
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## RESULT 6

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US-09-949-016-11750
; Sequence 11750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: February 4, 2005, 17:40:03 / Search time 618 Seconds

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Title: US-10-628-464-1

Perfect score: 957  
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Gapop 60.0, Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	20	2.1	686	US-03-770-149-317	Sequence 317, App
3	4	19	248	US-09-864-761-10004	Sequence 30004, A
4	19	2.0	263	US-09-864-761-19935	Sequence 19935, A
5	19	2.0	387	US-09-864-761-1156	Sequence 6952, Ap
6	19	2.0	404	US-10-242-535A-6952	Sequence 6952, Ap
7	19	2.0	404	US-10-085-783A-6952	Sequence 6952, Ap
8	19	2.0	479	US-10-027-632-179761	Sequence 179761, A
9	19	2.0	479	US-10-027-632-179762	Sequence 179762, A
10	19	2.0	479	US-10-027-632-179763	Sequence 179763, A
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C 13	19	2.0	479	17	US-10-027-632-179763	Sequence 179763, A
C 14	19	2.0	485	9	US-09-864-761-136	Sequence 136, App
C 15	19	2.0	536	9	US-09-864-761-13456	Sequence 13456, A
C 16	19	2.0	883	17	US-10-425-114-3651	Sequence 3651, Ap
C 17	19	2.0	1119	17	US-10-369-493-32521	Sequence 32521, A
C 18	19	2.0	1173	17	US-10-425-114-30814	Sequence 30814, A
C 19	19	2.0	1246	17	US-10-425-114-1158	Sequence 1158, Ap
C 20	19	2.0	1255	18	US-10-425-115-11535	Sequence 11535, A
C 21	19	2.0	1866	9	US-09-738-626-2199	Sequence 2199, Ap
C 22	19	2.0	2718	18	US-10-437-963-99200	Sequence 99200, A
C 23	19	2.0	2881	16	US-10-247-671-4	Sequence 4, Appl1
C 24	19	2.0	3570	10	US-09-964-295-3	Sequence 3, Appl1
C 25	19	2.0	3570	15	US-10-154-419-21	Sequence 21, Appl1
C 26	19	2.0	3746	9	US-09-834-975-762	Sequence 762, App
C 27	19	2.0	4059	17	US-10-120-988-316	Sequence 316, App
C 28	19	2.0	4163	17	US-10-291-265-583	Sequence 583, App
C 29	19	2.0	4163	17	US-10-291-265-584	Sequence 584, App
C 30	19	2.0	4205	17	US-10-291-265-111	Sequence 111, App
C 31	19	2.0	4295	17	US-10-291-265-112	Sequence 112, App
C 32	19	2.0	4541	17	US-10-297-633-11	Sequence 11, Appl
C 33	19	2.0	4633	10	US-09-964-295-1	Sequence 1, Appl1
C 34	19	2.0	4633	15	US-10-154-419-19	Sequence 19, Appl1
C 35	19	2.0	4971	17	US-10-332-447-36	Sequence 36, Appl1
C 36	19	2.0	4990	18	US-10-723-860-197	Sequence 197, Appl
C 37	19	2.0	4999	17	US-10-187-975-25	Sequence 25, Appl
C 38	19	2.0	5038	18	US-10-723-860-4939	Sequence 4939, Ap
C 39	19	2.0	5116	17	US-10-187-975-21	Sequence 21, Appl1
C 40	19	2.0	5335	17	US-10-187-975-19	Sequence 19, Appl1
C 41	19	2.0	5369	17	US-10-187-975-17	Sequence 17, Appl1
C 42	19	2.0	5566	17	US-10-187-975-23	Sequence 23, Appl1
C 43	19	2.0	5955	18	US-10-490-556-1	Sequence 1, Appl1
C 44	19	2.0	31923	18	US-10-490-556-3	Sequence 3, Appl1
C 45	19	2.0	3309400	9	US-09-738-626-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-628-464-1, Application US/10628464  
; Sequence 1, Appl1  
; Publication No. US2004012134A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; APPLICANT: TANG, HUIXIAN  
; APPLICANT: PRONIN, ALEXEY  
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
; FILE REFERENCE: 100317.54260US  
; CURRENT APPLICATION NUMBER: US/10/628.464  
; CURRENT FILING DATE: 2003-07-29  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 957  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(954)  
US-10-628-464-1

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 957; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 ATGAATGAGACACATGCTTCTAGATCTTCGGTACATGACAAAGGCCATCATCTTG 60  
DB GTTACCATTTTACTCTTCTTACCGCTGTAGATGACAGGAGGATGCTTCTTACTGCT 120  
61 GTTACCATTTTACTCTTCTTACCGCTGTAGATGACAGGAGGATGCTTCTTACTGCT 120  
DB GTTACCATTTTACTCTTCTTACCGCTGTAGATGACAGGAGGATGCTTCTTACTGCT 120

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QY	181	AGCCTAAGGGGCGCTTCGCTTCTGTGCTGCACTCAGTGGTAATGGGTAAAGACCATTTATGTT	240
Db	181	AGCCTAAGGGGCGCTTCGCTTCTGTGCTGCACTCAGTGGTAATGGGTAAAGACCATTTATGTT	240
QY	241	TTCTTGCATCCCATGGGCGCTTCCCATACAAACCCGTACTGAGATTTCTAGCTTTCAGTGG	300
Db	241	TTCTTGCATCCCATGGGCGCTTCCCATACAAACCCGTACTGAGATTTCTAGCTTTCAGTGG	300
QY	301	GACTTCCTGAATGCTGCCACCTTATGGTCCCTACCTGCTCAGTGTCTTCTATTTGGTG	360
Db	301	GACTTCCTGAATGCTGCCACCTTATGGTCCCTACCTGCTCAGTGTCTTCTATTTGGTG	360
QY	361	AAAAATTGCTACCTTCAACCCACCCCTGTCTTCTTGTGGCTAAAGACAAGTTGTCTGGGTGG	420
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QY	421	CTACCATGATGTCTCTCAAGCTCTGTAGGGGCTCCAGCTTCAACCATTTCTATTTTTC	480
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QY	481	ATAGGCAACCAAGATGTATCAGAACTATTTAAGNACCATATCAACCTTGGAAATGTC	540
Db	481	ATAGGCAACCAAGATGTATCAGAACTATTTAAGNACCATATCAACCTTGGAAATGTC	540
QY	541	ACTGGCGATAGCATACGAGAGCTACTGTAGAAATTTCTATTCTTCCCTCTAAAAATGATT	600
Db	541	ACTGGCGATAGCATACGAGAGCTACTGTAGAAATTTCTATTCTTCCCTCTAAAAATGATT	600
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Db	601	ACTTGGAACAATGCCCCACTGCTGCTTTTTCATTTGCAATGATTTTGTGCATCAATCTGTG	660
QY	661	GGAAGACACAGGAAGAAGGCTCTCCTTACAACTCAGATTCGAGAGCCAGTGTGCAG	720
Db	661	GGAAGACACAGGAAGAAGGCTCTCCTTACAACTCAGATTCGAGAGCCAGTGTGCAG	720
QY	721	GGACACATTAAGGCGCTGCTGGGCTCCCTCTTTTGGCCATGCTCTTCATCTCATATTTTC	780
Db	721	GGACACATTAAGGCGCTGCTGGGCTCCCTCTTTTGGCCATGCTCTTCATCTCATATTTTC	780
QY	781	CTGTACTACTGTATTCAGTGTCTGCAAGGTATTTTCCACTCTGACCTTTAAATTTCTGGGTG	840
Db	781	CTGTACTACTGTATTCAGTGTCTGCAAGGTATTTTCCACTCTGACCTTTAAATTTCTGGGTG	840
QY	841	TGGGAGTCAGTGATTTTATCTGTGTGACAGCATTCACCCCATCATTTGCTTCAAGCAAC	900
Db	841	TGGGAGTCAGTGATTTTATCTGTGTGACAGCATTCACCCCATCATTTGCTTCAAGCAAC	900
QY	901	TGCAGGCTAGAGGCTGTGCTGAAAGATCGCGTTCTCAAGAGTGTGGNACCTTTGA	957
Db	901	TGCAGGCTAGAGGCTGTGCTGAAAGATCGCGTTCTCAAGAGTGTGGNACCTTTGA	957

RESULT 2  
US-09-770-149-317/c  
Sequence 317, Application US/09770149  
Patent No. US20020059663A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameake, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Mathew, Abraham V.  
APPLICANT: Ledford, Brooke L.

```

APPLICANT: Moesener, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Ma'ja
APPLICANT: Slader, Ted
APPLICANT: Davis, Ketch R.
APPLICANT: Allen, Ketch
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/1178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: Faastsq for Windows Version 4.0
SEQ ID NO 317
LENGTH: 686
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-317

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Query Match	2.1%;	Score 20;	DB 9;	Length 666;
Best Local Similarity	100.0%;	Pred. No. 11;		
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			0;	Indels
				Gaps
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QY      429 GATGCTCTTCAGCTCTGTAG 448
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1  RESULT 3
2  US-09-864-761-30004/C
3  Sequence 30004, Application US/09864761
4  Patent No. US20020048763A1
5  GENERAL INFORMATION:
6  APPLICANT: Penn, Sharron G.
7  APPLICANT: Rank, David R.
8  APPLICANT: Hanzel, David K.
9  APPLICANT: Chen, Wensheng
10 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
11 FILE REFERENCE: Aeomica-X-1
12 FILE REFERENCE: Aeomica-X-1
13 CURRENT APPLICATION NUMBER: US/09/864,761
14 CURRENT FILING DATE: 2001-05-23
15 PRIOR APPLICATION NUMBER: US 60/180,312
16 PRIOR FILING DATE: 2000-02-04
17 PRIOR APPLICATION NUMBER: US 60/207,456
18 PRIOR FILING DATE: 2000-05-26
19 PRIOR APPLICATION NUMBER: US 09/632,366
20 PRIOR FILING DATE: 2000-08-03
21 PRIOR APPLICATION NUMBER: GB 24263.6
22 PRIOR FILING DATE: 2000-10-04
23 PRIOR APPLICATION NUMBER: US 60/236,359
24 PRIOR FILING DATE: 2000-09-27
25 PRIOR APPLICATION NUMBER: PCT/US01/00666
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00667
28 PRIOR FILING DATE: 2001-01-30
29 PRIOR APPLICATION NUMBER: PCT/US01/00664
30 PRIOR FILING DATE: 2001-01-30
31 PRIOR APPLICATION NUMBER: PCT/US01/00669
32 PRIOR FILING DATE: 2001-01-30
33 PRIOR APPLICATION NUMBER: PCT/US01/00665
34 PRIOR FILING DATE: 2001-01-30
35 PRIOR APPLICATION NUMBER: PCT/US01/00668
36 PRIOR FILING DATE: 2001-01-30
37 PRIOR APPLICATION NUMBER: PCT/US01/00663
38 PRIOR FILING DATE: 2001-01-30
39 PRIOR APPLICATION NUMBER: PCT/US01/00662
40 PRIOR FILING DATE: 2001-01-30

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:40:48 / Search time 3740 Seconds  
(without alignments)  
9739.975 Million cell updates/sec

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Scoring table: Oligo-NTC  
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: gb\_est2.\*  
3: gb\_est3.\*  
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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2.3	343	3	CNS0AAX3	EX818026 Arabidops
2	2.2	265	2	BF334145	BF334145 QVO-CT022
3	2.2	333	9	CR204857	CR204857 Forward s
4	2.2	421	2	BF334124	BF334124 QVO-CT022
5	2.2	690	9	CE385477	CE385477 tigr-g88-
6	2.2	770	8	B2703595	B2703595 PUCDM05TD
7	2.2	881	9	CU095884	CU095884 ISB1-27D3
8	2.1	154	9	CR134201	CR134201 Forward s
9	2.1	266	8	AQ423937	AQ423937 C17B1-B1-
10	2.1	399	5	BP636602	BP636602 BP636602
11	2.1	403	5	BP651637	BP651637 BP651637
12	2.1	407	1	AV806931	AV806931 AV806931
13	2.1	410	7	TT9009	TT9009 y421c10..f1
14	2.1	426	1	AV796617	AV796617 AV796617
15	2.1	429	1	BP584610	BP584610 BP584610
16	2.1	434	7	CN280406	CN280406 170005999
17	2.1	440	8	BH612499	BH612499 SALX 0328
18	2.1	457	5	BP594212	BP594212 BP594212
19	2.1	508	5	BQ334935	BQ334935 PM3-MT020
20	2.1	531	8	A2851897	A2851897 2M0154B21
21	2.1	539	1	AA042165	AA042165 24486 CD4
22	2.1	547	9	CG946784	CG946784 MBEHL04TR
23	2.1	571	1	AV442263	AV442263 AV442263
24	2.1	599	4	B0313552	B0313552 B0313552

C	25	20	2.1	635	7	CK121968	CK121968 211024.p1
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C	28	20	2.1	649	1	AU239214	AU239214 AU239214
C	29	20	2.1	695	7	CF127884	CF127884 UI-HF-ET0
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C	31	20	2.1	782	8	BH347499	BH347499 CH230-42E
C	32	20	2.1	834	5	CL662448	CL662448 PRI0141C
C	33	20	2.1	850	5	BU468832	BU468832 603370758
C	34	20	2.1	855	7	CO064460	CO064460 est_k_bre
C	35	20	2.1	867	7	CO919076	CO919076 AGENCOURT
C	36	20	2.1	889	9	CG975841	CG975841 MBEKH62TR
C	37	20	2.1	961	5	BQ734733	BQ734733 AGENCOURT
C	38	20	2.1	1036	9	CL287350	CL287350 ZMMBB063
C	39	20	2.1	1372	2	BE963287	BE963287 601656723
C	40	20	2.1	1689	3	CNS0915X	EX81567 Arabidops
C	41	20	2.0	174	1	AA677888	AA677888 z115902.s
C	42	19	2.0	174	2	BF847350	BF847350 CM3-EN004
C	43	19	2.0	241	4	BJ646546	BJ646546 BJ646546
C	44	19	2.0	251	7	CN925144	CN925144 000501AEN
C	45	19	2.0	256	2	B0330938	B0330938 B0330938

#### ALIGNMENTS

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LOCUS  
DEFINITION  
CNS0AAX3 343 bp mRNA linear HTC 06-FEB-2004  
Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
GSLTSL57E06 of Silique of strain col-0 of Arabidopsis thaliana  
(thale cress).

ACCESSION  
EX818026  
VERSION  
EX818026.1 GI:42470707  
KEYWORDS  
HTC; GSLL CDNA.  
SOURCE  
Arabidopsis thaliana  
ORGANISM  
Arabidopsis thaliana

REFERENCE  
AUTHORS  
Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J., Salanoubat,M., Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

#### TITLE

JOURNAL  
REFERENCE  
2 (bases 1 to 343)

AUTHORS  
TITLE  
JOURNAL  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

#### COMMENT

The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
USG INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information Center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length  
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

#### FEATURES

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 TCTTCTGGCTNAGCAGCAGTT 410  
Db 309 TCTTCTGGCTNAGCAGCAGTT 330

RESULT 2  
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LOCUS BF334145  
DEFINITION QV0-CT0225-280700-307-e09 CT0225 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF334145  
VERSION BF334145.1 GI:11304893  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0225-280700-307-e09&t3=2000-07-28&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 19  
High quality sequence stop: 264.

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 GCTTCTGTCTGCAGTCAGTGG 217  
Db 238 GCTTCTGTCTGCAGTCAGTGG 258

RESULT 3  
CR204857 333 bp DNA linear GSS 06-JUL-2004  
LOCUS CR204857  
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN144p22, genomic survey sequence.  
ACCESSION CR204857  
VERSION CR204857.1 GI:49983706  
KEYWORDS GSS; genome survey sequence; MICE.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.  
TITLE Direct Substitution  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgehire, CB10 1SA, UK. http://www.sanger.ac.uk/MICE  
LOCATION/Qualifiers 1. 333  
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## FEATURES

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 308 ATGACAGCAATGGCTTCATC 328

RESULT 4  
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LOCUS BF334124  
DEFINITION QV0-CT0225-191199-058-c08 CT0225 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF334124  
VERSION BF334124.1 GI:11304872  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 / Search time 168 Seconds  
(without alignments)  
732.082 Million cell updates/sec

Title: US-10-628-464-2

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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1: geneseqp1980s:\*  
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3: geneseqp2000s:\*  
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5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	960	57.2	312	6 ABR58013	ABr58013 Mouse GI
5	609	36.3	307	5 AAU11389	AAu11389 Human T2R
6	609	36.3	307	5 ABP95935	ABP95935 Human GPC
7	609	36.3	307	7 ADC86989	ADc86989 Human GPC
8	609	36.3	307	8 ADR29250	ADr29250 Taste rec
9	608	36.2	307	8 ADM33293	Adm33293 Human bit
10	597.5	35.6	308	4 AAB87820	AAb87820 Mouse T2R
11	597.5	35.6	308	4 AAB87792	AAb87792 Taste rec
12	589.5	35.1	308	4 AAB87160	AAb87160 Rat T2R12
13	589.5	35.1	308	4 ABR58017	ABr58017 Taste rec
14	425	25.3	294	6 ABR58017	ABr58017 Rat GI en
15	416	24.8	291	8 ADM33329	Adm33329 Human bit
16	409	24.4	298	6 ABR58014	ABr58014 Mouse GI
17	408	24.3	291	4 AAB87746	AAb87746 Human T2R
18	408	24.3	291	8 ADJ84511	ADj84511 Human T2R
19	408	24.3	291	6 ADR29091	ADr29091 Taste rec
20	402.5	24.0	293	6 ABR58012	ABr58012 Mouse GI
21	378.5	22.6	318	4 AAB87737	AAb87737 Human T2R
22	378.5	22.6	318	8 ADJ84494	ADj84494 Human T2R
23	378.5	22.6	318	8 ADQ17322	ADq17322 Human sof
24	378.5	22.6	318	8 ADQ17199	ADq17199 Human sof
25	378.5	22.6	318	8 ADR29074	ADr29074 Taste rec

26	378.5	22.6	318	8 ADM33317	Adm33317 Human bit
27	371	22.1	299	4 AAB87812	AAb87812 Mouse T2R
28	371	22.1	299	4 ADR29200	ADr29200 Taste rec
29	359	21.4	312	4 AAB87739	AAb87739 Human T2R
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31	359	21.4	312	8 ADR29078	ADr29078 Taste rec
32	359	21.4	312	8 ADM33321	Adm33321 Human bit
33	356	21.2	299	4 AAB87783	AAb87783 Rat T2R03
34	356	21.2	299	8 ADJ84452	ADj84452 Rat T2R G
35	356	21.2	299	8 ADR29142	ADr29142 Taste rec
36	345.5	20.6	312	6 ABR58015	ABr58015 Rat GI en
37	344.5	20.5	297	4 AAB87786	AAb87786 Rat T2R06
38	344.5	20.5	297	8 AAB87746	AAb87746 Taste rec
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41	339	20.2	321	8 ADR29236	ADr29236 Taste rec
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#### ALIGNMENTS

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AC AAU98514;  
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DT 24-SEP-2002 (first entry)  
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DE Novel human G-protein coupled receptor.  
XX  
KW G-protein coupled; receptor; liver; central nervous system disease;  
KW Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;  
KW hyperlipaemia; cancer; non-small cell lung cancer; ovarian cancer;  
KW stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;  
KW circulatory disease; hypertension; atherosclerosis; angina; allergy;  
KW inflammatory disease; respiratory disease; asthma; bronchitis;  
KW digestive disease; stomach ulcer; duodenal ulcer; immune disorder;  
KW autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;  
KW pneumonia; influenza.  
XX  
XX Homo sapiens.  
XX  
XX WO200257309-A1.  
XX  
XX PD 25-JUL-2002.  
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XX PF 17-JAN-2002; 2002WO-JP000271.  
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XX PR 18-JAN-2001; 2001JP-00010814.  
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XX PR 30-MAR-2001; 2001JP-00102558.  
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XX PA (TAKAE ) TAKEDA CHEM IND LTD.  
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XX PI Miwa M, Ito T, Shintani Y, Miyajima N;  
XX WPI: 2002-538457/57.  
XX DR N-PSDB; ABR58014.  
XX  
XX PT New G-protein coupled receptor protein expressed in human liver for  
XX design of drugs and reagents for treatment and diagnosis of cancer and  
XX respiratory metabolic and other diseases.  
XX  
XX PS Claim 1; Page 89-91; 101pp; Japanese.  
XX  
XX CC The invention describes a novel G-protein coupled receptor protein  
XX expressed in human liver. The protein is used in the treatment,  
XX prevention and diagnosis of central nervous system diseases (such as  
XX Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes

CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
 CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
 CC circulatory diseases (such as hypertension, atherosclerosis and angina),  
 CC inflammatory diseases (such as allergy and rheumatism), respiratory  
 CC diseases (such as asthma and bronchitis), digestive diseases (such as  
 CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
 CC diseases), and infections (such as acquired immunodeficiency syndrome  
 CC (AIDS), pneumonia and influenza). This is the amino acid sequence of the  
 CC novel G-protein coupled receptor protein described in the invention  
 XX

Sequence 318 AA:

Query Match 100.0%; Score 1678; DB 5; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFTTALGVEWTLRRMLPCDKLTV 60  
 DB 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFTTALGVEWTLRRMLPCDKLTV 60  
 QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLMSSTWLSVFYCV 120  
 DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLMSSTWLSVFYCV 120  
 QY 121 KIATFTHPVFVFLKHLKSGWLPWMLFSSVGLSFTTILFFIGNHRMYQNTLRNHLQPMNV 180  
 DB 121 KIATFTHPVFVFLKHLKSGWLPWMLFSSVGLSFTTILFFIGNHRMYQNTLRNHLQPMNV 180  
 QY 181 TGSISRYCEKFFLPLKMTWTMPYAVFICMILLITSLGRRKKALLTTSGRFSPVQ 240  
 DB 181 TGSISRYCEKFFLPLKMTWTMPYAVFICMILLITSLGRRKKALLTTSGRFSPVQ 240  
 QY 241 AHKALLALISFAMLFISYFLSVFSAAGIFPPLDFKFWWESVYILCAAVHPILLFSN 300  
 DB 241 AHKALLALISFAMLFISYFLSVFSAAGIFPPLDFKFWWESVYILCAAVHPILLFSN 300  
 QY 301 CRLRAVLKSRSSRCGTP 318  
 DB 301 CRLRAVLKSRSSRCGTP 318

RESULT 2  
 ADJ87105 standard; protein; 318 AA.

AC ADJ87105;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Amino acid sequence of human bitter taste receptor T2R76.  
 XX  
 KM Human, bitter taste receptor; T2R76; chromosome 7; bitter taste.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004011617-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 29-JUL-2003; 2003WO-US023604.  
 XX  
 PR 29-JUL-2002; 2002US-0398727P.  
 XX  
 PA (SENO-) SENOMYX INC.  
 PA (ADLER-) ADLER J E.  
 PA (TANG-) TANG H.  
 PA (PRON-) PRONIN A.  
 PA (ZOLL-) ZOLLER M.  
 XX  
 PI Adler JE, Tang H, Pronin A, Zoller M;  
 DR WPI, 2004-143845/14.  
 DR N-PSDB; ADJ87104.

XX Novel isolated bitter taste receptor, T2R76 polypeptide useful for  
 PT identifying modulators of taste perception, or bitter compounds.  
 XX  
 PS Claim 5; Page 98-100; 100pp; English.

CC The present sequence represents human bitter taste receptor T2R76. The  
 CC human T2R76 gene is located on chromosome 7 in the region 144062692-  
 CC 144063648. The reading frame of T2R76 is intronless. T2R76 polypeptides  
 CC and polynucleotides are useful for identifying modulators. Such  
 CC modulators are useful for modulating bitter taste perception in a  
 CC subject. T2R76 agonists can be administered to enhance bitter tastes,  
 CC while T2R76 antagonists can be administered to reduce bitter taste.  
 XX

Sequence 318 AA:

Query Match 100.0%; Score 1678; DB 8; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFTTALGVEWTLRRMLPCDKLTV 60  
 DB 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFTTALGVEWTLRRMLPCDKLTV 60  
 QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLMSSTWLSVFYCV 120  
 DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLMSSTWLSVFYCV 120  
 QY 121 KIATFTHPVFVFLKHLKSGWLPWMLFSSVGLSFTTILFFIGNHRMYQNTLRNHLQPMNV 180  
 DB 121 KIATFTHPVFVFLKHLKSGWLPWMLFSSVGLSFTTILFFIGNHRMYQNTLRNHLQPMNV 180  
 QY 181 TGSISRYCEKFFLPLKMTWTMPYAVFICMILLITSLGRRKKALLTTSGRFSPVQ 240  
 DB 181 TGSISRYCEKFFLPLKMTWTMPYAVFICMILLITSLGRRKKALLTTSGRFSPVQ 240  
 QY 241 AHKALLALISFAMLFISYFLSVFSAAGIFPPLDFKFWWESVYILCAAVHPILLFSN 300  
 DB 241 AHKALLALISFAMLFISYFLSVFSAAGIFPPLDFKFWWESVYILCAAVHPILLFSN 300  
 QY 301 CRLRAVLKSRSSRCGTP 318  
 DB 301 CRLRAVLKSRSSRCGTP 318

RESULT 3  
 ADM33335 standard; protein; 318 AA.

AC ADM33335;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human bitter taste receptor TAS2R60 protein SEQ ID NO:49.  
 XX  
 KM human, bitter taste receptor; food.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004029087-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-EP010691.  
 XX  
 PR 25-SEP-2002; 2002US-0413298P.  
 XX  
 PA (DEER-) DEUT INST ERNAERHUNGSFORSCHUNG POTSDAM.  
 XX  
 PI Bufer B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
 DR WPI, 2004-305149/28.  
 DR N-PSDB; ADM33336.

XX Novel bitter receptor polynucleotide encoding human TAS2R protein having  
PT bitter substance binding activity, useful for producing nutraceutical or  
PT pharmaceutical compositions comprising antagonists of bitter taste  
receptor activity.  
PS Claim 14; SEQ ID NO 49; 108bp; English.  
XX  
CC The present sequence represents a human bitter taste receptor. Also  
CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
CC a vector (II) containing (I); (3) a host cell (III) genetically  
CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
CC acid sequence encoded by (I) or obtained by culturing (III) and  
CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
CC isolating (MI) a compound that binds to (V) encoded by (I); (10)  
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
CC foodstuff including human and animal foodstuff, any precursor material or  
CC additive employed in the production of foodstuff comprising (VIII) and  
CC (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an  
CC active agent and optionally a carrier. (III) is useful for producing a  
CC polypeptide encoded by (I), which involves culturing (III) and recovering  
CC the polypeptide encoded by (I). (II) is useful for producing cells  
CC capable of expressing at least one of the bitter taste receptor  
CC polypeptide, which involves genetically cells in vitro with (II), where  
CC the bitter taste receptor polypeptide(s) is (are) encoded by (I). (MI) or  
CC (M2) can be used for producing food or any precursor material or additive  
CC employed in the production of foodstuffs. (MI) or (M2) can also be used  
CC for producing nutraceutical or pharmaceutical compositions. (I), (II),  
CC (VI) or (VIII) can be used for manufacturing a medicament for the  
CC treatment of an abnormally increased or decreased sensitivity towards a  
CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminates bitter tasting components of food and effectively useful in  
CC food industries.  
XX  
SQ Sequence 318 AA;  
Query Match 100.0%; Score 1678; DB 8; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGDHMYLGSSVTDKKAIIVTLLRLVAIAAGNGFTTALGVEWTLRMLPDCDLY 60  
DB 1 MNGDHMYLGSSVTDKKAIIVTLLRLVAIAAGNGFTTALGVEWTLRMLPDCDLY 60  
QY 61 SLGASRECLQSVVMGKTIYVFLHMAFPYVQLFLAFQMDFLNAATLMSSTWLSVFCV 120  
DB 61 SLGASRECLQSVVMGKTIYVFLHMAFPYVQLFLAFQMDFLNAATLMSSTWLSVFCV 120  
QY 121 KIATFHPVFPWMLKHLKSGMLPWWLFSVGLSFTTILFFIGNHRMYQNYLRNLQPMNV 180  
DB 121 KIATFHPVFPWMLKHLKSGMLPWWLFSVGLSFTTILFFIGNHRMYQNYLRNLQPMNV 180  
QY 181 TGSBSIRYCEKFTYLPKMTWTWMPTRVAFICMLILITSLGRHKKALLTSGRRESVQ 240  
DB 181 TGSBSIRYCEKFTYLPKMTWTWMPTRVAFICMLILITSLGRHKKALLTSGRRESVQ 240  
QY 241 AHIKALALISFAMLFISYFLSVFSAAGIFPPIDFKFWWESYIYCAAVHPITLFSN 300  
DB 241 AHIKALALISFAMLFISYFLSVFSAAGIFPPIDFKFWWESYIYCAAVHPITLFSN 300  
QY 301 CRLRAVLKSRSSRCGTP 318  
DB 301 CRLRAVLKSRSSRCGTP 318  
RESULT 4  
ABRS8013  
ID ABR58013 standard; protein; 312 AA.  
XX

AC ABR58013;  
XX  
XX 25-JUL-2003 (first entry)  
DT  
XX  
DE Mouse GI endocrine cell specific GPCR GT2R-m39.  
XX  
KM Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;  
KM gastrointestinal tract; taste; enteroendocrine cell.  
XX  
OS Mus musculue.  
XX  
XX WO2003031604-A1.  
PN  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002MO-US032664.  
XX  
XX 12-OCT-2001; 2001US-0328933P.  
PR  
XX (REGC ) UNIV CALIFORNIA.  
PA (PHLE/) PHLEGER C S W.  
XX  
XX Welsh JH, Rozengurt JE, Wu SV;  
PI WPI; 2003-381713/36.  
DR N-PSDB; ACC44449.  
DR  
XX  
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,  
PT useful for identifying chemical sensing receptors and signaling molecules  
PT that allow pharmacological and genetic modulation of taste transduction  
PT pathways.  
XX  
PS Disclosure; Page 63-64; 101bp; English.  
XX  
XX This sequence represents a novel isolated chemosensing G-protein coupled  
CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic  
CC acid is useful for identifying or isolating chemical sensing receptors  
CC (including taste ion channels) and signaling molecules that would allow  
CC pharmacological and genetic modulation of taste transduction pathways.  
CC The native STC-1 enteroendocrine cells that naturally express GT2R are  
CC useful in identifying modulators of taste receptor-mediated signal  
CC transduction. These cells are also used as models for studying taste-  
CC mediated signal transduction  
XX  
SQ Sequence 312 AA;  
Query Match 57.2%; Score 960; DB 6; Length 312;  
Best Local Similarity 58.8%; Pred. No. 1.4e-97;  
Matches 181; Conservative 46; Mismatches 81; Indels 0; Gaps 0;  
QY 1 MNGDHMYLGSSVTDKKAIIVTLLRLVAIAAGNGFTTALGVEWTLRMLPDCDLY 60  
DB 1 MNGDHMYLGSSVTDKKAIIVTLLRLVAIAAGNGFTTALGVEWTLRMLPDCDLY 60  
QY 61 SLGASRECLQSVVMGKTIYVFLHMAFPYVQLFLAFQMDFLNAATLMSSTWLSVFCV 120  
DB 61 SLGASRECLQSVVMGKTIYVFLHMAFPYVQLFLAFQMDFLNAATLMSSTWLSVFCV 120  
QY 121 KIATFHPVFPWMLKHLKSGMLPWWLFSVGLSFTTILFFIGNHRMYQNYLRNLQPMNV 180  
DB 121 KIATFHPVFPWMLKHLKSGMLPWWLFSVGLSFTTILFFIGNHRMYQNYLRNLQPMNV 180  
QY 181 TGSBSIRYCEKFTYLPKMTWTWMPTRVAFICMLILITSLGRHKKALLTSGRRESVQ 240  
DB 181 TGSBSIRYCEKFTYLPKMTWTWMPTRVAFICMLILITSLGRHKKALLTSGRRESVQ 240  
QY 241 AHIKALALISFAMLFISYFLSVFSAAGIFPPIDFKFWWESYIYCAAVHPITLFSN 300  
DB 241 AHIKALALISFAMLFISYFLSVFSAAGIFPPIDFKFWWESYIYCAAVHPITLFSN 300  
QY 301 CRLRAVLK 308  
DB 301 PVLRAVLK 308



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OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 ; Search time 22 Seconds  
(without alignments)  
1079.018 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MNQDHWLVGSSVTDKKAIL.....SNGRLRAVLKRRSSRGTP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUS COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	24.8	291	4	US-09-949-016-8213 Sequence 8213, Ap
2	408	24.3	291	4	US-09-393-634-64 Sequence 64, Appl
3	408	24.3	291	4	US-09-949-016-6919 Sequence 6919, Ap
4	378.5	22.6	318	4	US-09-393-634-47 Sequence 47, Appl
5	378.5	22.6	318	4	US-09-949-016-9253 Sequence 9253, Ap
6	359	21.4	312	4	US-09-393-634-51 Sequence 51, Appl
7	356	21.2	299	4	US-09-393-634-5 Sequence 5, Appl
8	337.5	20.1	309	4	US-09-393-634-49 Sequence 49, Appl
9	336	20.0	299	4	US-09-393-634-35 Sequence 35, Appl
10	332.5	19.8	316	4	US-09-393-634-39 Sequence 39, Appl
11	332.5	19.8	316	4	US-09-949-016-8207 Sequence 8207, Ap
12	329.5	19.6	302	4	US-09-393-634-37 Sequence 37, Appl
13	319.5	19.0	335	4	US-09-393-634-1 Sequence 1, Appl
14	304	18.1	300	4	US-09-393-634-58 Sequence 58, Appl
15	293	17.5	299	4	US-09-393-634-43 Sequence 43, Appl
16	293	17.5	299	4	US-09-949-016-6942 Sequence 6942, Ap
17	293	17.5	299	4	US-09-949-016-8156 Sequence 8156, Ap
18	283	16.9	300	4	US-09-393-634-17 Sequence 17, Appl
19	279	16.6	300	4	US-09-393-634-19 Sequence 19, Appl
20	273.5	16.3	307	4	US-09-393-634-53 Sequence 53, Appl
21	266	15.9	310	4	US-09-393-634-7 Sequence 7, Appl
22	264.5	15.8	299	4	US-09-393-634-41 Sequence 41, Appl
23	254	15.1	300	4	US-09-393-634-62 Sequence 62, Appl
24	241.5	14.4	315	4	US-09-393-634-56 Sequence 56, Appl
25	240.5	14.3	333	4	US-09-393-634-3 Sequence 3, Appl
26	231.5	13.8	317	4	US-09-393-634-60 Sequence 60, Appl
27	212.5	12.7	266	4	US-09-393-634-15 Sequence 15, Appl

28	200.5	11.9	224	4	US-09-393-634-9 Sequence 9, Appl
29	152.5	9.1	209	4	US-09-393-634-13 Sequence 13, Appl
30	151.5	9.0	121	4	US-09-393-634-70 Sequence 70, Appl
31	145.5	8.7	173	4	US-09-393-634-23 Sequence 23, Appl
32	140.5	8.4	180	4	US-09-393-634-33 Sequence 33, Appl
33	134	8.0	115	4	US-09-393-634-27 Sequence 27, Appl
34	131	7.8	144	4	US-09-393-634-66 Sequence 66, Appl
35	129.5	7.7	155	4	US-09-393-634-21 Sequence 21, Appl
36	123.5	7.4	129	4	US-09-393-634-72 Sequence 72, Appl
37	121	7.2	126	4	US-09-393-634-31 Sequence 31, Appl
38	120	7.2	355	4	US-09-170-496D-2 Sequence 2, Appl
39	120	7.2	355	4	US-09-170-496D-164 Sequence 164, Appl
40	117.5	7.0	450	4	US-09-721-870-16 Sequence 16, Appl
41	116.5	6.9	359	2	US-08-467-568-13 Sequence 27, Appl
42	116.5	6.9	359	2	US-08-467-568-13 Sequence 13, Appl
43	116.5	6.9	359	2	US-08-103-170-2 Sequence 4, Appl
44	116.5	6.9	359	2	US-09-030-582-13 Sequence 2, Appl
45	116.5	6.9	359	3	US-09-171-456-19 Sequence 19, Appl

## ALIGNMENTS

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RESULT 1
US-09-949-016-8213
; Sequence 8213, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8213
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8213

Query Match      24.8% Score 416; DB 4; Length 291;
Best Local Similarity 32.1%; Pred. No. 4.4e-32;
Matches 94; Conservative 55; Mismatches 134; Indels 10; Gaps 3;

QY      18 IIVTLLRLRLVAAGNGFITAALGVEWVLRMLPCDILVSLGASRECLQSVWGKT 77
      8 VFMIITVLESLLTIYQSSILVAVLGRWLVQVRLMPVMDILSLGSRCLQWASLNLN 67
QY      78 IYVFLHPMAPVPVPIQFLAFQWDFLNAATLWSSTLVSFYCYKIAITFTVPVFLKHL 137
      68 FCSY-----FNILNVVVCNLTITWIEFNILTFWINSILTYFYCYKISVFTFHIFLWLRRI 122
QY      138 SGWLPMMVLSSVGLSFTTILFFIGNHMYQVNLRLHQLQPMWNTGSSINSYCKPFLEPL 197
      123 LRLFPMLGLSLMTTCVTIIPSAIGNYIQIQLTMEHLPRNSTVTKLENFHO--YQFOA 180
QY      198 KMITWMPVAVFICMLILITSLGRKRALTTSGFRSPVOAHTKALIALSPMLFPI 257
      181 HTVAIVIPFLFLASTIFLMASTL---TKIQHSHSTHCNCPMKAAHTALRSIAVLFIVFT 237
QY      258 SYLSLVFSAAGIFPPIDFEKWTWESVIYCAAVPIILFNSCRILPAVLKSR 310
      238 SYFLTLITITIGTLFDKRCWLWWEAFYVAFILMSTSLMSSPTLKRILKXK 290
DB
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2005, 17:02:31 ; Search time 132 Seconds

(without alignments)  
784.647 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MNGDHWLGSSTVDKKAII.....SNCRRLAVLKRSSRCRGP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
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19: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	318	16	US-10-628-464-2
2	609	36.3	307	9	US-09-825-882-18
3	609	36.3	307	14	US-10-017-161-1786
4	609	36.3	307	15	US-10-292-798-1442
5	609	36.3	307	10	US-10-343-650A-680
6	597.5	35.6	308	15	US-09-510-332-155
7	589.5	35.1	308	10	US-09-510-332-99
8	408	24.3	291	9	US-09-393-634-64
9	408	24.3	291	10	US-09-510-332-30
10	408	24.3	291	14	US-10-383-982-64
11	378.5	22.6	318	9	US-10-364-861-64
12	378.5	22.6	318	9	US-09-393-634-47
13	378.5	22.6	318	10	US-09-510-332-13

14	378.5	22.6	318	14	US-10-383-982-47	Sequence 47, Appl
15	378.5	22.6	318	15	US-10-364-861-47	Sequence 47, Appl
16	371	22.1	299	10	US-09-510-332-139	Sequence 139, Appl
17	359	21.4	312	9	US-09-393-634-51	Sequence 51, Appl
18	359	21.4	312	10	US-09-510-332-17	Sequence 17, Appl
19	359	21.4	312	14	US-10-383-982-51	Sequence 51, Appl
20	359	21.4	312	15	US-10-364-861-51	Sequence 51, Appl
21	356	21.2	299	9	US-09-393-634-51	Sequence 51, Appl
22	356	21.2	299	10	US-09-510-332-81	Sequence 81, Appl
23	356	21.2	299	14	US-10-383-982-5	Sequence 5, Appl
24	356	21.2	299	15	US-10-364-861-5	Sequence 5, Appl
25	344.5	20.5	297	10	US-09-510-332-87	Sequence 87, Appl
26	339	20.2	321	9	US-09-825-882-4	Sequence 4, Appl
27	339	20.2	331	15	US-10-292-798-1732	Sequence 1732, Ap
28	339	20.2	331	14	US-10-017-161-1786	Sequence 2086, Ap
29	339	20.2	338	14	US-10-017-161-2140	Sequence 2140, Ap
30	339	20.2	338	15	US-10-292-798-1786	Sequence 1786, Ap
31	339	20.2	338	15	US-10-343-650A-676	Sequence 676, App
32	338	20.1	338	15	US-10-343-650A-678	Sequence 678, App
33	337.5	20.1	309	9	US-09-393-634-49	Sequence 49, Appl
34	337.5	20.1	309	10	US-09-510-332-15	Sequence 15, Appl
35	337.5	20.1	309	14	US-10-383-982-49	Sequence 49, Appl
36	337.5	20.1	309	15	US-10-364-861-49	Sequence 49, Appl
37	336.5	20.1	332	10	US-09-510-332-162	Sequence 162, App
38	336	20.0	299	9	US-09-393-634-35	Sequence 35, Appl
39	336	20.0	299	10	US-09-510-332-35	Sequence 35, Appl
40	336	20.0	299	14	US-10-383-982-35	Sequence 35, Appl
41	336	20.0	299	15	US-10-364-861-35	Sequence 35, Appl
42	332.5	19.8	316	9	US-09-393-634-39	Sequence 39, Appl
43	332.5	19.8	316	10	US-09-510-332-5	Sequence 5, Appl
44	332.5	19.8	316	14	US-10-383-982-39	Sequence 39, Appl
45	332.5	19.8	316	15	US-10-364-861-39	Sequence 39, Appl

#### ALIGNMENTS

RESULT 1  
US-10-628-464-2  
Sequence 2, Application US/10628464  
Publication No. US2004012134A1  
GENERAL INFORMATION:  
APPLICANT: ADLER, JON ELLIOT  
APPLICANT: TANG, HUIXIAN  
APPLICANT: PRONIN, ALEXEY  
TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
FILE REFERENCE: 100337.54260US  
CURRENT APPLICATION NUMBER: US/10/628,464  
CURRENT FILING DATE: 2003-07-29  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 3.2  
SEQ ID NO 2  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-628-464-2

Query Match 100.0%; Score 1678; DB 16; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.8e-144;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNGDHWLGSSTVDKKAIIIVTLLLRVAINGRFTALGVENVLRMLPCDGLV	60
DB	1	MNGDHWLGSSTVDKKAIIIVTLLLRVAINGRFTALGVENVLRMLPCDGLV	60
QY	61	SLGSRFCLOSVMGKTIYVFLHPMAFPYVLOFLAFQWDPLNAATLWSSTLVSFVCV	120
DB	61	SLGSRFCLOSVMGKTIYVFLHPMAFPYVLOFLAFQWDPLNAATLWSSTLVSFVCV	120
QY	121	KIATFTPVFPMWKHKLISGMLPMMLFSSVGLSFTTTLFTGHRMYONTLRNHLQPMNV	180
DB	121	KIATFTPVFPMWKHKLISGMLPMMLFSSVGLSFTTTLFTGHRMYONTLRNHLQPMNV	180

Oy	181	TGGSISYCEKFFLPFLKMIWTMPRAVAFICMILLITSLGHRKKALLTSGRRESVQ	240
Db	181	TGGSIRYCEKFFLPFLKMIWTMPRAVAFICMILLITSLGHRKKALLTSGRRESVQ	240
Oy	241	AHKAIIALALSFMELTSYFSLVFSASAIGPPLDPKRWMEVSYYLCAAVHPILILPSN	300
Db	241	AHKAIIALALSFMELTSTYFSLVFSASAGPPLDPKRWMEVSYYLCAAVHPILILPSN	300
Oy	301	CRLRAVLTKSRSSRCGTP	318
Db	301	CRLRAVLTKSRSSRCGTP	318

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US-09-825-882-18
RESULT 2
US-09-825-882-18
: Sequence 18, Application US/09825882
: Patent No. US20020094551A1
: GENERAL INFORMATION:
: APPLICANT: ADLER, JON ELLIOT
: TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
: FILE REFERENCE: 078003/0279152/RXT
: CURRENT APPLICATION NUMBER: US/09/825, 882
: CURRENT FILING DATE: 2001-04-05
: PRIOR APPLICATION NUMBER: 60/195,532
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: 60/247,014
: PRIOR FILING DATE: 2000-11-13
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 18
: LENGTH: 307
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-825-882-18

```

Query Match	36.3%	Score 609;	DB 9;	Length 307;
Best Local Similarity	41.9%	Pred. No. 3.5e-47;		
Matches 122;	Conservative 46;	Mismatches 111;	Indels 12;	Gaps 2

```

QY      2  VTTLLLRLLVAINGNEPTAALGVEVNLARMYLLPCDCLVLSGAREFGLSGVMGKITYV  80
Db      10  VLFSLSLLEGTIANNGFIYVLQREMLRARGRLRPDMLILISIGASRFCLQVLGVYVHPY  69
QY      81  FLHPMAEPYNPVLQFLAFQMDFLNAATLSSTWLSVFCYCVKIATFTHPFWMKHLKSGW  140
Db      70  SAQKVEKSGCGLQGFPHLHNHFNLSATPFCSCMLSLTFCVKIANTHTSTPLMLKRPFGW  129
QY      141  LPMMLLFSVGLSSFTLLRFLPFGNHRKQYUHL-----RHHQCPMNTGSIKSYCEKYYLF  199
Db      130  VPMMLLGSVLISITITLLFFPMVWVRYQDFLLRKFSGNMTYKWN-----TRLETYYFP  182
QY      196  PLKMTITWMTAVAFPICMILLITSLGRHKKALLTTSGRREPSVQAHIKALLALSLFAML  255
Db      183  SLKLVISIFSFVFLVSIIMLLINSLRHHQGRQMHGHSIDQPSQAHTRALKSLISFLIL  242
QY      256  FISTFLSVLSANGIRPRLDFKFWKVESYIYICAAVHPILLFNSCRKRAV  306
Db      243  YALSFSLILDAAKFIQMDQFWPQIQLVLCISVHPRIILLFSLMKLRASV  293

```

RESULT 3  
 US-10-017-161-1786  
 \* Sequence 1786, Application US/1001761  
 \* Publication No. US2003014368A1  
 \* GENERAL INFORMATION:  
 \* APPLICANT: SUMA, MAKIO  
 \* APPLICANT: ASAI, KIYOSHI  
 \* APPLICANT: AKIYAMA, YUTAKA  
 \* APPLICANT: ABURATANI, HIROYUKI  
 \* TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
 \* FILE REFERENCE: 084335/0152  
 \* CURRENT APPLICATION NUMBER: US/10/017,161  
 \* CURRENT FILING DATE: 2002-12-18

```

? PRIOR APPLICATION NUMBER: JP 2001/246785
? PRIOR FILING DATE: 2001-06-16
? NUMBER OF SEQ. ID NOS: 2430
? SOFTWARE: PatentIn Ver. 2.1
? SEQ. ID NO. 1786
? LENGTH: 307
?
? TYPE: PRT
? ORGANISM: Homo sapiens
?
? US-10-017-161-1786

```

Query Match 36.3%; Score 609; DB 14; Length 307;

Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;

```

QY      21 VITLLILRLVALAGNGFTIILAAQVEMVLRRLMLICDCKLVLISGSRCLDSVVMGKTIYV  80
DQ      10 VLLFSLSLSLGILAAAGFIYLVGREMLAKYGRLLPLDMLILISLGSARCLDQVGVNHFY  69
QY      81 FLHPEMAPPPNPVLQGLAFQMDPLNATLMSSTWLSVFYCYKIAFTHPVFFMLKHLKSGW  140
DQ      70 SAQKVFSSGGLRGOFHLHMLHPLNLSATWFCMSLISVLFQVCKIANITSTFLMLKMRPPGW  129
QY      141 LPMLPESSVGGLSSFTLLIFFTIGNHMYQNYL-----RNHLQPMNVATGDSIRSYCEKRYLF  195
DQ      130 VPMLLGSLVLSFIITLLEFFWNYVYVQEFILRPSGMYTKM-----TRLEITYFP  182
QY      196 PLKMITWPTPAVFICIMILLITSLGRRKAKALLTSGSFREPSVOAHIKALLALSFAML  255
DQ      183 SLKTLVMSIPSFVFLVIMTLINSLRRRTQRMQNHGSLADPSTQATRALKSLISPLL  242
QY      256 FIFIFSLVFSANAQIPPLDQFKFWMSVETIYCAVHPITLLFENCLTRAV  306
DQ      243 VALSFSLIIDAQKFSMQNDQVMAQVLAVALCTSVHPFLIFSNLKLRSV  293

```

RESULT 4  
US-10-292-798-1442  
; Sequence 1442, Application US/10292798  
; Publication No. US2003023583A1  
Journal of Invention

```

1  APPLICANT: SUMA, MAKIKO
2  APPLICANT: ASAI, KIYOSHI
3  APPLICANT: AKIYAMA, YUTAKA
4  APPLICANT: ABURAYAN, HIROYUKI
5  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
6  FILE REFERENCE: 084335/166
7  CURRENT APPLICATION NUMBER: US/10/292,798
8  CURRENT FILING DATE: 2002-11-13
9  PRIOR APPLICATION NUMBER: 10/017,161
10 PRIOR FILING DATE: 2001-12-18
11 PRIOR APPLICATION NUMBER: JP 2001-246789
12 PRIOR FILING DATE: 2001-06-18
13 NUMBER OF SEQ ID NOS: 2070
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 1442
16     LENGTH: 307
17     TYPE: PRT
18     ORGANISM: Homo sapiens
19     US-10-292-798-1442

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	Query Match	36.3%	Score 609	DB 15	Length 307
	Best Local Similarity	41.9%	Pred. No. 3.56-47		
	Matches 122	Conservative 46	Mismatches 111	Indels 12	Gaps 21
Qy	VTIILLRLVIAINGFTTALGVEWTLRRMLRCDKLVLVSLGSRFCLQSVMMGKTIYV	80			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Db	10 VLRLSLSLGLIANGRFVLVYGRKWRIRYGLDLDMILISLGASRFCLQVGVVHNRY	69			
Qy	81 FLHMAEPYNPVLTQFLAFQMDFLNAATLWSTLVSEFCVIAIAFTFHPVFWMLKLGSGM	140			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Db	70 SAQKVEYSGGLGRFPFLHMHFLNLSAIFWPCSWLSVLEFCVIAIAITHTSTFLMLKMRFCGM	129			
Qy	141 LPWMLFSSVGLSFTTILFPIGIRHMYQNYL-----RNHLPQMPNVGTGDSIRSCEKFLYLF	195			

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 ; Search time 39 Seconds  
(without alignments)  
784.537 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678  
Sequence: 1 MNGDHMVLGSSVTDKAIL.....SNCRRLRAVLKSRSSRCGTP 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Database :

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PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*
```

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	141.5	8.4	376	2	A48157	opsin, ocular - <i>R</i>
2	139.5	8.3	376	2	B48157	opsin, lateral eye
3	131.5	7.8	376	2	S28583	opsin - red swamp
4	127	7.6	381	1	OOFF2	opsin 2 - fruit fl
5	121.5	7.2	381	2	S40622	opsin rh2 - fruit
6	120	7.2	355	2	A55753	G protein-coupled
7	117.5	7.0	539	2	T27559	hypothetical prot
8	117	7.0	338	2	T32116	hypothetical prot
9	116.5	6.9	359	2	JH0449	histamine H2 recepe
10	116.5	6.9	374	2	S40691	opsin rh1 - fruit
11	115	6.9	373	1	COFF	rhodopsin - fruit
12	114.5	6.8	350	2	T25156	hypothetical prot
13	114.5	6.8	352	2	T25155	hypothetical prot
14	114.5	6.8	364	2	A3821	serotonin receptor
15	112	6.7	337	2	JC5821	neurotransmitter r
16	110.5	6.6	398	2	JN0708	thyrotropin-releasa
17	110	6.6	384	2	AF0636	glucans biosynthes
18	109	6.5	305	2	B69548	molybdopterin oxid
19	109	6.5	393	2	A39251	thyrotropin-relea
20	108.5	6.5	310	2	T61758	pheromone receptor
21	108.5	6.5	352	2	A45757	neuropeptide y/pep
22	107	6.4	394	2	T31891	hypothetical prot
23	106.5	6.3	347	1	C46137	opsin, violet-sens
24	106.5	6.3	352	2	G00048	opsin, violet-sens
25	106.5	6.3	353	2	S28757	opsin (LESTRA) - c
26	106	6.3	365	2	AB1566	neuropeptide y/pep
27	105	6.3	411	2	T56444	thyrotrophin-relea
28	105	6.3	412	2	S23436	thyrotrophin recepe
29	105	6.3	432	2	H64383	Na+ transporter -

## ALIGNMENTS

30	104.5	6.2	377	2	A53279	serotonin receptor
31	104	6.2	780	2	T23555	hypothetical prote
32	103	6.1	341	2	T09800	NADH dehydrogenas
33	103	6.1	380	2	A55259	kappa opiod recept
34	102.5	6.1	344	2	T12247	NADH dehydrogenas
35	102.5	6.1	359	2	JC4120	histamine H2 recep
36	102.5	6.1	516	2	T33269	hypothetical prote
37	102	6.1	359	2	S15403	angiotensin II recep
38	102	6.1	371	2	A39234	opsin - bluebottled
39	102	6.1	1162	2	E84431	proble Na+/H+ an
40	101.5	6.0	346	2	UC5715	G protein-coupled
41	101	6.0	358	2	UQ1278	histamine H2 recep
42	101	6.0	380	2	JC3338	kappa opiod recept
43	101	6.0	380	2	A48227	kappa opiod recept
44	100.5	6.0	342	2	T22192	hypothetical prote
45	100.5	6.0	374	2	I77467	serotonin receptor

## RESULT 1

opsin, ocellular Atlantic horseshoe crab  
C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
C:Date: 17-Jul-1994 #sequence revision 17-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A48197  
R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993  
A:Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus  
A:Reference number: A48197; MUID:93317641; PMID:8327495  
A:Accession: A48197  
A:Status: preliminary  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-376 <SWI>  
A:Cross-references: UNIPROT:P3361; EMBL:L03792; NID:g156644; PIDN:AAA28374.1; PID:g156644  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; retinal  
E:318/Binding site: retinal (Lys) (covalent) #status predicted

Query Match	8.4%	Score 141.5;	DB 2;	Length 376;	.
Best Local Similarity	18.8%;	Pred. No. 0.00017;			
Matches 68;	Conservative 62;	Mismatches 110;	Indels 121;	Gaps 16	

[illegible]

## RESULT 2

B48197

opsin, lateral eye - Atlantic horseshoe crab

C:Species: Limulus polyphemus (Atlantic horseshoe crab)

C&gt;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004

C/Accession: B48197

R/Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993

A&gt;Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus

A/Reference number: A48197; MUID:93317641; PMID:8327495

A/Accession: B48197

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-376 &lt;SMI&gt;

A/Cross-references: UNIPROT:P35360; EMBL:L03791; NID:g156642; PIDN:AAA28273.1; PID:g1566

C:Superfamily: vertebrate rhodopsin

C/Keyword: chromoprotein, G protein-coupled receptor, lipoprotein, photoreceptor, retinal

F/18/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 8.3%; Score 139.5; DB 2; Length 376;

Best Local Similarity 19.8%; Pred. No. 0.00025;

Matches 67; Conservative 64; Mismatches 134; Indels 71; Gaps 16;

QY 19 ILVTLLRLVAIAGNGFTTALGVWYLRMLPCDKLIVSLGASRFLQSVV--GKT 77

DB 49 ILGVAMIIIGIICVIGNGVYVLMYTKSLR---TPNLLVNLAFSDFCMAFMPTWT 105

QY 78 IYVFLHMAF-PYNPVLOFLAFQWDFLNAATLWSSTWLS-----VFCVKIATFTHP-- 128

DB 106 SNGFAEHWILGPF--KEVYVGMAGSLFCGASIMSMWITLDRNNVYRGMAAPLTHKKA 163

QY 129 ----VFVFWLQKLSGMLPMLFSSVGLSFTTLLFPIGNHMYQNYLRNHQPMNVYTGDS 184

DB 164 TLILLFWIMS--GGM-----TLIPFGWGR-----YVPSGNTLSCT 198

QY 185 I-----RSYCKEFLFLPKMTWTMPTRVFTICMILLTSGRHKR-----ALL 229

DB 199 VDLITLDMSSASVYVYIGLAVLPFLPTMYCYFFIYHAVAHEHKQLREQAKKNVASLR 258

QY 230 TTSGFPRSVQAHKLLALLSFAMLFISYFLSVPSAAGIF-----PPLDFKFWWES 283

DB 259 ANADQKQSHACGL-AKVAMMTVGLMWTMTPTLIISMAVFSGSTRLTPL---ATTGGS 314

QY 284 VYVLC-AAVPIILFSSNCRRLRAVLKSR-RSSRCGT 317

DB 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

RESULT 3

S28853

opsin - red swamp crayfish

C:Species: Procambarus clarkii (red swamp crayfish)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S28853

R/Hariyama, T.; Ozaki, K.; Tokunaga, F.; Tsukahara, Y.

FEBS Lett. 315, 287-292, 1993

A>Title: Primary structure of crayfish visual pigment deduced from cDNA.

A/Reference number: S28853; MUID:93138090; PMID:8422920

A/Accession: S28853

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-376 <NR>

A/Cross-references: UNIPROT:P35356; GB:S53494; NID:g263969; PIDN:AA25036.1; PID:g263970

C:Superfamily: vertebrate rhodopsin

C/Keyword: chromoprotein, lipoprotein, retinal

F/21/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 376;

Best Local Similarity 20.8%; Pred. No. 0.0012;

Matches 72; Conservative 60; Mismatches 105; Indels 109; Gaps 18;

QY 19 ILVTLLRLVAIAGNGFTTALGVWYLRMLPCDKLIVSLGASRFLQSVV-- 73

DB 49 ILGVAMIIIGIICVIGNGVYVLMYTKSLR---TPNLLVNLAFSDFCMAFMPTWT 105

QY 78 IYVFLHMAF-PYNPVLOFLAFQWDFLNAATLWSSTWLS-----VFCVKIATFTHP-- 128

DB 106 SNGFAEHWILGPF--KEVYVGMAGSLFCGASIMSMWITLDRNNVYRGMAAPLTHKKA 163

QY 129 ----VFVFWLQKLSGMLPMLFSSVGLSFTTLLFPIGNHMYQNYLRNHQPMNVYTGDS 184

DB 164 TLILLFWIMS--GGM-----TLIPFGWGR-----YVPSGNTLSCT 198

QY 185 I-----RSYCKEFLFLPKMTWTMPTRVFTICMILLTSGRHKR-----ALL 229

DB 199 VDLITLDMSSASVYVYIGLAVLPFLPTMYCYFFIYHAVAHEHKQLREQAKKNVASLR 258

QY 230 TTSGFPRSVQAHKLLALLSFAMLFISYFLSVPSAAGIF-----PPLDFKFWWES 283

DB 259 ANADQKQSHACGL-AKVAMMTVGLMWTMTPTLIISMAVFSGSTRLTPL---ATTGGS 314

QY 284 VYVLC-AAVPIILFSSNCRRLRAVLKSR-RSSRCGT 317

DB 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

QY 315 VFAKANSVYPIYVIGISHPRYKALYGRPSLACGS 350

DB 55 LLLIFMLFTGILCLAGN-FVYI-----WVPNTKSLRTPANLLVNLANSDFLMTMP 108

QY 74 -----MGKT-----IYVFL-----HPMAF-----PYNVLOFLAFQWDFLNA 105

DB 109 PMNVTCYHTWTLGPFQCVYVAFNLGCGCASIWTMTVFTLPRNNVYVGVAGEPLSTKK 168

QY 106 ATWMSST-NLSYFCVKIATFTHPVFFLKHKLSCMLPMLFSSVGLSSFTTILEFTGN 163

DB 169 ASIMLITIVLSTWICIA-----PFGNNRYVPEGNL-----TGCCTD-----YLSE 210

QY 164 HRNYQNYLNNHLPNNVTDSDIRSCEKRYFLPKMTWTMPTRVFTICMILLTSLGHN 223

DB 211 DIISRSYLYD-----YSTWVYLPLEP-----YCVSTIKAVAAH 246

QY 224 RKXALLTSGFPRSVQAHKAL-----LALLSFAMLFISYFLSVPSA 267

DB 247 EK-----GMDQAKMGITKISRNEAKTSAECLAKIANTYVLAHWIATWPIYLLHW 299

QY 268 AGIIPP--LDFKFWESVYVLCVAH-PILLFSSNCRRLRAVLKSR 310

DB 300 VGMFARSYLSPYVTIYGVPFAKANAVYNDIYVAISHPRYKAAEMKK 345

RESULT 4

OOF2

opsin 2 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C/Accession: A24058

R/Coman, A.F.; Zuker, C.S.; Rubin, G.M.

Cell 44, 705-710, 1986

A>Title: An opsin gene expressed in only one photoreceptor cell type of the Drosophila

A/Reference number: A24058; MUID:86133563; PMID:2936466

A/Accession: A24058

A/Molecule type: DNA

A/Residues: 1-381 <COM>

A/Cross-references: UNIPROT:P08099; GB:M12896; NID:g158009; PIDN:AAA28734.1; PID:g158010

C:Comment: This protein is specifically expressed in photoreceptor cell R8 of the Drosophila

C/Genetic:

A/Gene: Rh2

A/Cross-references: FlyBase:FBgn0003248

A/Map position: 3R (91D-2)

A/Intons: 33/3, 339/2, 350/3

C:Superfamily: vertebrate rhodopsin

C/Keyword: chromoprotein, G protein-coupled receptor, photoreceptor, retinal; transmembrane

F/1-56/Domain: extracellular #status predicted <EX1>

F/57-81/Domain: transmembrane #status predicted <TM1>

F/82-93/Domain: intracellular #status predicted <IM1>

F/94-116/Domain: transmembrane #status predicted <TM2>

F/117-134/Domain: extracellular #status predicted <EX2>

F/135-160/Domain: transmembrane #status predicted <TM3>

F/161-167/Domain: intracellular #status predicted <IM2>

F/168-188/Domain: transmembrane #status predicted <TM4>

F/189-222/Domain: extracellular #status predicted <EX3>

F/223-250/Domain: transmembrane #status predicted <TM5>

F/251-283/Domain: intracellular #status predicted <IM3>

F/284-307/Domain: transmembrane #status predicted <TM6>

F/308-315/Domain: extracellular #status predicted <EX4>

F/316-339/Domain: transmembrane #status predicted <TM7>

F/340-381/Domain: intracellular #status predicted <IM4>

F/382-381/Domain: intracellular #status predicted

Query Match 7.6%; Score 127; DB 1; Length 381;

Best Local Similarity 20.6%; Pred. No. 0.0028;

Matches 73; Conservative 48; Mismatches 109; Indels 124; Gaps 16;

QY 19 ILVTLLRLVAIAGNGFTTALGVWYLRMLPCDKLIVSLGASRFL---GSVWVG 75

DB 59 ILGLFLTAIITISCCNGVYVIFGSTR---TPANLLVNLAFSDFCMAFSQSPVM- 114

QY 76 KTIYVFLHMAF-PYNPVLOFLAFQWDFLNAATLWSSTWLS---SVFCVKIATFTHPV-- 130

DB 115 -----IINFYETVWL---GPLMCDIYAGCGSLFCGVSIMSMCMIAFDR 155

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 ; Search time 63 Seconds

(without alignments)  
2584.781 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MNGDHWLVSSVTDKKAIL.....SNCRRAVLKRRSRRCGTP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	318	1 TR60 HUMAN	P59551 homo sapien
2	1638	97.6	318	2 06465T	064655 pan troglod
3	1630	97.1	318	2 0646D0	064660 pan paniscu
4	1622	96.7	318	2 064520	064520 gorilla gor
5	1514	90.2	318	2 0645U7	0645U7 pongo pygma
6	1480	88.2	318	2 0645S2	0645S2 macaca mula
7	960	57.2	312	1 TR35 MOUSE	07TQ89 mus musculu
8	953	56.8	321	2 067BE2	067BE2 rattus norv
9	608	36.2	307	1 TR41 HUMAN	P59536 homo sapien
10	607	36.2	307	2 0646B2	0646B2 pan troglod
11	600	35.8	307	2 0646C7	0646C7 pan paniscu
12	597.5	35.6	308	1 T2RC MOUSE	P59532 mus musculu
13	597.5	35.6	308	2 07M704	07M704 mus musculu
14	596	35.5	307	2 0645Y3	0645Y3 gorilla gor
15	589.5	35.1	308	1 T2RC RAT	07JKE0 rattus norv
16	580	34.6	307	2 0645U6	0645U6 pongo pygma
17	560	33.4	307	2 0645S8	0645S8 macaca mula
18	560	33.4	307	2 0646F3	0646F3 papio hamad
19	431	25.7	291	2 0645U1	0645U1 pongo pygma
20	427	25.4	298	1 TR34 MOUSE	07TQ80 mus musculu
21	425	25.3	294	2 067BE3	067BE3 rattus norv
22	423	25.2	291	2 0646B3	0646B3 pan troglod
23	421	25.1	291	2 0645Y4	0645Y4 gorilla gor
24	421	25.1	291	2 0646E7	0646E7 papio hamad
25	419	25.0	291	2 0646A6	0646A6 pan troglod
26	418.5	24.9	329	2 0646D1	0646D1 pan paniscu
27	418.5	24.9	329	2 067BE7	067BE7 rattus norv
28	416	24.8	291	2 0645W1	0645W1 homo sapien
29	415	24.7	291	2 0645S3	0645S3 macaca mula
30	408	24.3	291	1 T2RG HUMAN	09NYV7 homo sapien
31	402.5	24.0	293	1 TR43 MOUSE	07TQ89 mus musculu

32	379.5	22.6	318	2 0645T7	0645T7 macaca mula
33	378.5	22.6	318	1 T2R7 HUMAN	09NYV3 homo sapien
34	378.5	22.6	319	2 0646C4	0646C4 pan troglod
35	378.5	22.6	319	2 0646D6	0646D6 pan paniscu
36	377.5	22.5	317	2 0646F6	0646F6 papio hamad
37	376.5	22.4	318	2 0646A2	0646A2 gorilla gor
38	374.5	22.3	318	2 0645V8	0645V8 pongo pygma
39	371	22.1	299	1 T2R3 MOUSE	P59529 mus musculu
40	371	22.1	299	2 07M728	07M728 mus musculu
41	362	21.6	311	2 0645T0	0645T0 macaca mula
42	359	21.4	312	1 T2R9 HUMAN	09NYV1 homo sapien
43	358	21.3	312	2 0645W9	0645W9 homo sapien
44	357	21.3	299	1 T2R1 CERAE	08MJU6 cercopithec
45	357	21.3	311	2 0646G5	0646G5 papio hamad

#### ALIGNMENTS

RESULT 1  
TR60 HUMAN STANDARD; PRT; 318 AA.  
ID TR60 HUMAN  
AC P59551; Q7RTR7;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Taste receptor type 2 member 60 (TR60).  
GN Name=TR60;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22471936; PubMed=12584440; DOI=10.1159/000068546;  
RA Conte C., Ebelling M., Marcuz A., Nef P., Andres-Barguin P. J.;  
RT "Identification and characterization of human taste receptor genes  
belonging to the TAS2R family";  
RL Cytogenet. Genome Res. 98:45-53(2002).  
RN [2]  
RP REVIEW.  
RX MEDLINE=2213574; PubMed=12139882; DOI=10.1016/S0959-4388(02)00345-8;  
RA Montmayeur J.-P., Matsunami H.;  
RT "Receptors for bitter and sweet taste";  
RL Curr. Opin. Neurobiol. 12:366-371(2002).  
RN [3]  
RP REVIEW.  
RX MEDLINE=21634924; PubMed=11696554; DOI=10.1074/jbc.R100054200;  
RA Margolskee R.F.;  
RT "Molecular mechanisms of bitter and sweet taste transduction";  
RL J. Biol. Chem. 277:114(2002).  
RN [4]  
RP REVIEW.  
RX MEDLINE=22469025; PubMed=12581520; DOI=10.1016/S0092-8674(03)00071-0;  
RA Zhang Y., Hoon M.A., Chandrasekar J., Mueller K.L., Cook B., Wu D.,  
Zaker C.S., Ryba N.J.;  
RT "Coding of sweet, bitter, and umami tastes: different receptor cells  
sharing similar signaling pathways";  
RL Cell 112:293-301(2003).  
RN [5]  
RP PHYLOGENETIC ANALYSIS.  
RX MEDLINE=2258047; PubMed=12679530; DOI=10.1093/molbev/mg083;  
RA Shi P., Zhang Y., Yang H., Zhang Y.P.;  
RT "Adaptive diversification of bitter taste receptor genes in Mammalian  
evolution";  
RL Mol. Biol. Evol. 20:805-814(2003).  
CC -1- FUNCTION: Receptor that may play a role in the perception of  
bitterness and is gustducin-linked. May play a role in sensing the  
chemical composition of the gastrointestinal content. The activity  
of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
activation and lead to the gating of TRPM5 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells

CC of the tongue and exclusively in gustducin-positive cells.  
 CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited  
 CC number of bitter compounds; individual taste cells can  
 CC discriminate among bitter stimuli.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.  
 CC -----  
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 CC -----  
 CC EMBL: AY114094; AAM63544.1; -;  
 CC EMBL: BK001100; DA01207.1; -;  
 CC Genew: HGNC:20639; TAS2R60.  
 CC InterPro: IPR007960; TAS2\_Recept.  
 CC DR Pfam: PF05296; TAS2R; 1.  
 CC DR G-protein coupled receptor; Receptor; Transmembrane.  
 CC KW DOMAIN 1 7  
 CC FT TRANSMEM 1 8  
 CC FT TRANSMEM 29 40  
 CC FT TRANSMEM 41 61  
 CC FT TRANSMEM 62 88  
 CC FT TRANSMEM 89 109  
 CC FT TRANSMEM 110 128  
 CC FT TRANSMEM 129 149  
 CC FT TRANSMEM 150 183  
 CC FT TRANSMEM 184 204  
 CC FT TRANSMEM 205 234  
 CC FT TRANSMEM 235 255  
 CC FT TRANSMEM 256 264  
 CC FT TRANSMEM 265 285  
 CC FT CARBOHYD 179 179  
 CC FT SEQUENCE 318 AA; 36336 MW; DEDABIIC81017648 CRC64;  
 CC  
 CC Query Match 100.0%; Score 1678; DB 1; Length 318;  
 CC Best Local Similarity 100.0%; Pred. No. 4.1e-116;  
 CC Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
 DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
 QY 121 KIATFHPVFPFLKHLKSLGMLPFWLFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
 DB 121 KIATFHPVFPFLKHLKSLGMLPFWLFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
 QY 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 DB 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 QY 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 DB 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 QY 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWESVITYCAAVHPITILFSN 300  
 DB 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWESVITYCAAVHPITILFSN 300  
 QY 301 CRRLAVLKSRRSSRCGTP 318  
 DB 301 CRRLAVLKSRRSSRCGTP 318

RESULT 2  
 ID 0646A5 PRELIMINARY; PRT; 318 AA.  
 AC 0646A5;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Taste receptor T2R56.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Anne F., Yoav G., Orna M., Svante P.;  
 RT "Evolution of bitter taste receptors in human and apes."  
 RL Submitted (Aug-2004) to the EMBL/Genbank/DBD databases.  
 DR EMBL: AY724901; AAU21114.1; -;  
 KW RECEPTOR.  
 SQ SEQUENCE 318 AA; 36411 MW; 3DBB9FAC7A8A330 CRC64;  
 CC  
 CC Query Match 97.6%; Score 1638; DB 2; Length 318;  
 CC Best Local Similarity 97.5%; Pred. No. 3.7e-113;  
 CC Matches 310; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
 DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
 QY 121 KIATFHPVFPFLKHLKSLGMLPFWLFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
 DB 121 KIATFHPVFPFLKHLKSLGMLPFWLFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
 QY 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 DB 181 TGSINSYCEKFFLPFKMTITWPTAVFFICMILITSLGRHKKALLTSGFRSPSVQ 240  
 QY 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWESVITYCAAVHPITILFSN 300  
 DB 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWESVITYCAAVHPITILFSN 300  
 QY 301 CRRLAVLKSRRSSRCGTP 318  
 DB 301 CRRLAVLKSRRSSRCGTP 318

RESULT 3  
 ID 0646D0 PRELIMINARY; PRT; 318 AA.  
 AC 0646D0;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Taste receptor T2R56.  
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9597;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Anne F., Yoav G., Orna M., Svante P.;  
 RT "Evolution of bitter taste receptors in human and apes."  
 RL Submitted (Aug-2004) to the EMBL/Genbank/DBD databases.  
 DR EMBL: AY724866; AAU21089.1; -;  
 KW RECEPTOR.  
 SQ SEQUENCE 318 AA; 36438 MW; 2658D7CDEB80C4C1 CRC64;  
 CC  
 CC Query Match 97.1%; Score 1630; DB 2; Length 318;  
 CC Best Local Similarity 97.2%; Pred. No. 1.5e-112;  
 CC Matches 309; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVENVLRMLPCDKLIV 60  
 QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
 DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNVLOFLAFQWDFLNAATLWSSTWLSVFCV 120



```

Db      61 SLGASHRCLOSVMGKTIYVFLYPMAPXYPNVQLFLPQMDFLMAATLMSWTLSVYCV 120
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      301 CRRLAVLKSRSSRCGTP 318
      301 CRRLAVLKSRSSRCGTP 318

```

## RESULT 4

064520 PRELIMINARY; PRT; 318 AA.

```

ID      064520
AC      064520;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Gorilla gorilla (gorilla).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX      NCBI_TaxId=9593;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY724923; AAU21129.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36275 MW; 57DF5AC0369F48E7 CRC64;

```

Query Match  
Best Local Similarity 96.7%; Score 1622; DB 2; Length 318;  
Matches 307; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

      1 MNGDHVLTGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVEWLRMLPCDKLLV 60
      1 MNGDHVLTGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVEWLRMLPCDKLLV 60
      61 SLGASHRCLOSVMGKTIYVFLHMAPPPNPVQLFLPQMDFLMAATLMSWTLSVYCV 120
      61 SLGASHRCLOSVMGKTIYVFLHMAPPPNPVQLFLPQMDFLMAATLMSWTLSVYCV 120
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      301 CRRLAVLKSRSSRCGTP 318
      301 CRRLAVLKSRSSRCGTP 318

```

RESULT 5  
064507 PRELIMINARY; PRT; 318 AA.

```

AC      064507;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Pongo pygmaeus (Orangutan).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX      NCBI_TaxId=9600;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY724986; AAU21172.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36554 MW; D0F6A7F44C3B5FA CRC64;

```

Query Match  
Best Local Similarity 90.2%; Score 1514; DB 2; Length 318;  
Matches 289; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

```

      1 MNGDHVLTGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVEWLRMLPCDKLLV 60
      1 MNGDHVLTGSSVTDKKAIIIVTILLRLVAIAGNGFTTALGVEWLRMLPCDKLLV 60
      61 SLGASHRCLOSVMGKTIYVFLHMAPPPNPVQLFLPQMDFLMAATLMSWTLSVYCV 120
      61 SLGASHRCLOSVMGKTIYVFLHMAPPPNPVQLFLPQMDFLMAATLMSWTLSVYCV 120
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      121 KIATFTPVVFWMLKHKLKSGMLPWWLFSSVGLSFTTILFFIGNHRMTQNTLRHLOPMNV 180
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      181 TGSIRSCEKFFYLPLKMITWMTPTAVFICMILLITSLGRHKKALLTSGFRPSVQ 240
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      241 AHKALALLSPFALFISYFLSLVFSAAAGIFPPDPKFWWESVYILCAAVHPITILLFSN 300
      301 CRRLAVLKSRSSRCGTP 318
      301 CRRLAVLKSRSSRCGTP 318

```

## RESULT 6

064552 PRELIMINARY; PRT; 318 AA.

```

ID      064552
AC      064552;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
OX      NCBI_TaxId=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY725022; AAU21197.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36278 MW; 15C342163F8F387B CRC64;

```

Query Match  
Best Local Similarity 88.2%; Score 1480; DB 2; Length 318;  
Matches 285; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

```
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DB 1 MNGDHWLVSSVTDKKAIIIVTLLRLVAIANGFTTALGVEVNLARMLLPCDKLIV 60
QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSTWLSVFCV 120
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QY 121 KIATFHPVFWLKHKLSCWLPWMLFSSVGLSFTTILFFIGNHRYONYLRNHLQPMNV 180
DB 121 KIATFHPVFWLKHKLSCWLPWMLFSSVGLSFTTILFFIGNHRYONYLRNHLQPMNV 180
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DB 181 TGDSTSYCEKFFLFPKMTITMTPTAVFICMILLITSLGRRKKALLTTSGRFSPSVQ 240
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DB 241 AHKALLALSPFALFISYFLSVFSAAGIFPPLDPKFWWESVLYCAVHPILLFNSN 300
QY 301 CRIRAVLKSRSSRCRTP 318
DB 301 CRIRAVLKSRSSRCRTP 318
QY 301 RRLRAVLIERCRSSRCRTP 318
DB 301 RRLRAVLIERCRSSRCRTP 318

RESULT 7
TR35 MOUSE STANDARD; PRT; 312 AA.
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AC 07T0A9; 07M705;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative taste receptor type 2 member 35 (TR35) (mT2r38).
GN Name=Taazr35; Synonym=Ta2r38;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN 1)
RC STRAIN=C57BL/6J;
RX MEDLINE=22709097; PubMed=12734386;
RY DOI=10.1152/physiolgenomics.00060.2003;
RA Conte C., Ebelling M., Marcuz A., Neff P., Andres-Barguin P., J.;
RT "Evolutionary relationships of the Taazr receptor gene families in
RT mouse and human.";
RL Physiol. Genomics 14:73-82(2003).
RN 12)
RP SEQUENCE FROM N.A.
RG The mouse genome sequencing consortium;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN 3)
RX GENE STRUCTURE.
RX MEDLINE=2255804; PubMed=12679530; DOI=10.1093/molbev/mg083;
RA Shi P., Zhang Y., Yang H., Zhang Y.-P.;
RT "Adaptive diversification of the bitter taste receptor genes in mammalian
RT evolution.";
RL Mol. Biol. Evol. 20:805-814(2003).
CC -1- FUNCTION: Putative taste receptor which may play a role in the
CC perception of bitterness.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF532786; AAP4036.1; ALT SEQ.
DR EMBL; CA001174173; -. NOT ANNOTATED_CDS.
DR EMBL; BK001097; DAA01236.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0008527; F:taste receptor activity; NAS.
DR GO; GO:0001580; P:perception of bitter taste; sensory transdu. .; NAS.
DR InterPro; IPR007960; TAs2_recept.
DR Pfam; PF05296; TAs2R; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT DOMAIN 1
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FT DOMAIN 41 66
FT DOMAIN 67 87
FT DOMAIN 88 97
FT DOMAIN 98 118
FT DOMAIN 119 140
FT DOMAIN 141 161
FT DOMAIN 162 198
FT TRANSMEM 199 219
FT TRANSMEM 220 244
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Query Match 57.2%; Score 960; DB 1; Length 312;
Best Local Similarity 58.8%; Pred. No. 4, 2e-63;
Matches 181; Conservative 46; Mismatches 81; Indels 0; Gaps 0;

QY 1 MNGDHWLVSSVTDKKAIIIVTLLRLVAIANGFTTALGVEVNLARMLLPCDKLIV 60
DB 1 MNGDHWLVSSVTDKKAIIIVTLLRLVAIANGFTTALGVEVNLARMLLPCDKLIV 60
QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSTWLSVFCV 120
DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSTWLSVFCV 120
QY 121 KIATFHPVFWLKHKLSCWLPWMLFSSVGLSFTTILFFIGNHRYONYLRNHLQPMNV 180
DB 121 KIATFHPVFWLKHKLSCWLPWMLFSSVGLSFTTILFFIGNHRYONYLRNHLQPMNV 180
QY 181 TGDSTSYCEKFFLFPKMTITMTPTAVFICMILLITSLGRRKKALLTTSGRFSPSVQ 240
DB 181 TGDSTSYCEKFFLFPKMTITMTPTAVFICMILLITSLGRRKKALLTTSGRFSPSVQ 240
QY 241 AHKALLALSPFALFISYFLSVFSAAGIFPPLDPKFWWESVLYCAVHPILLFNSN 300
DB 241 AHKALLALSPFALFISYFLSVFSAAGIFPPLDPKFWWESVLYCAVHPILLFNSN 300
QY 301 CRIRAVLK 308
DB 301 PVLRAVLK 308

RESULT 8
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ID 06TES2;
AC 06TES2;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative taste receptor T2R28.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN 1)
RP SEQUENCE FROM N.A.
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 4, 2005, 18:46:03 : Search time 4917 Seconds  
(without alignments)  
3133.772 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MGDHMYIGSSVTDKKAIL.....SNCRLRAVLKRRSRRCGTP 318

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1678	100.0	954	6	BD185566 Novel G p
3	1678	100.0	957	6	CQ738424 Sequence
4	1678	100.0	957	6	CQ800046 Sequence

5	1678	100.0	957	9	AY114094
6	1678	100.0	957	9	AY724955 Homo sapi
7	1678	100.0	72045	9	AC092214 Homo sapi
8	1638	97.6	957	9	AY724901 Pan trogl
9	1630	97.1	957	9	AY724866 Pan panis
10	1622	96.7	957	9	AY724923 Gorilla g
11	1514	90.2	957	9	AY724986 Pongo pyg
12	1480	88.2	957	9	AY725022 Macaca mu
13	960	57.2	966	10	AF532786 Mus muscu
14	960	57.2	203639	2	AC117625 Mus muscu
15	953	56.8	966	10	AY362748 Rattus no
16	953	56.8	218921	2	AC097912 Rattus no
17	609	36.3	924	6	BD144615 Novel G-p
18	609	36.3	924	6	CQ738419 Sequence
19	609	36.3	924	6	AY114093 Homo sapi
20	609	36.3	1324	6	AX647249 Sequence
21	609	36.3	175228	2	AC143343 Homo sapi
22	609	36.3	200123	9	AC073264 Homo sapi
23	608	36.2	921	6	CQ800004 Sequence
24	608	36.2	924	9	AF494232 Homo sapi
25	608	36.2	924	9	AY724956 Homo sapi
26	607	36.2	924	9	AY724891 Pan trogl
27	600.5	35.8	3437	6	AX097850 Sequence
28	600	35.8	924	9	AY724869 Pan panis
29	596	35.5	924	9	AY724933 Gorilla g
30	593.5	35.4	1295	6	AX097794 Sequence
31	593.5	35.4	223179	2	AC128080 Rattus no
32	589.5	35.1	927	10	AF240768 Rattus no
33	580	34.6	924	9	AY724987 Pongo pyg
34	560	33.4	924	9	AY724831 Papio ham
35	560	33.4	924	9	AY725013 Macaca mu
36	461	27.5	131565	2	AC143122 Macaca mu
37	431	25.7	876	2	AY724993 Pongo pyg
38	427.5	25.5	186051	2	EX005324 Mus muscu
39	427.5	25.5	200574	10	BX005304 Mouse DNA
40	427	25.4	80574	10	AF532785 Mus muscu
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42	423	25.2	876	9	AY724890 Pan trogl
43	422	25.1	876	9	AY724929 Gorilla g
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#### ALIGNMENTS

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LOCUS	BD171274				
DEFINITION	Novel G protein-coupled receptor protein and DNA thereof.				
ACCESSION	BD171274.1	GI:27877086			
VERSION	BD171274.1	GI:27877086			
KEYWORDS	WO 02057309-A/1.				
SOURCE	WO 02057309-A/1.				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 954)				
AUTHORS	Miwa, M., Ito, T., Shintani, Y. and Miyajima, N.				
TITLE	Novel G protein-coupled receptor protein and DNA thereof				
JOURNAL	Patent: WO 02057309-A 1 25-JUL-2002				
COMMENT	TAKEEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA				
OS	Homo sapiens (human)				
PN	WO 02057309-A/1				
PD	25-JUL-2002				
PR	17-JAN-2002 WO 2002JP000271				
PC	18-JAN-2001 JP 01P 010814, 30-MAR-2001 JP 01P 102558 PI				
PC	MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA				
PC	CQ7K16/28, CQ7K16/28, C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC				
PC	C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC				
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Alignment Scores:  
Pred. No.: 5,39e-142 Length: 954  
Score: 1678.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-10-628-464-2 (1-318) x BD171274 (1-954)

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5 AlaLeuGIyAaIyGtValLeuAaGArgMeIleuProCySaPlybLeuLeuVal 60  
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12 GACTTCTGAATGCTGCACTTATGTCTCTACCGCTCAGTGTCTTCTTATTTGTGTC 360  
13 LysIleAlaThrPheThrIaPhePhePhePhePhePhePhePhePhePhePhe 140  
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15 LeuProTTrpMetLeuPheSerSerValGIyLeuSerSerPheThrIlePhePhe 160  
16 CTACCAATGATGCTTCACTGCTGTGAGGCTCTCCAGCTTCAACCAATTTTCTTTC 480  
17 IleGIyAaNIaIaIaThrLeuTrpSerThrTrpLeuSerValPheYrCybVal 180  
18 ATAGGCAACCAACCAATGTATCAAGAACTATTAAAGAACATTTCAACCTTGAATGTC 540  
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24 GGAAGACACAGGAAGAGCTCTCTTACAACTCAGAGATTTCCAGAGGCCCACTGTGACG 720  
25 AlaNIaIleYbYsaIaLeuLeuAaIaLeuLeuSerPheAlaMetLeuPheIleSerYrPhe 260

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Score: 1678.00 Matches: 318  
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US-10-628-464-2 (1-318) x BD185566 (1-954)

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8 AGCTTACGGGCGCTCTGCTCTGTCTGCACTGAGTGAAGGTAAGCAATTTATGTT 240  
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10 TTTTGCATGCGAATGCGCTTCCCAATACCCCTGACTGCAATTTTCACTTCCAGTGG 300  
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13 LysIleAlaThrPheThrIaPhePhePhePhePhePhePhePhePhePhePhe 140  
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15 LeuProTTrpMetLeuPheSerSerValGIyLeuSerSerPheThrIlePhePhe 160  
16 CTACCAATGATGCTTCACTGCTGTGAGGCTCTCCAGCTTCAACCAATTTTCTTTC 480  
17 IleGIyAaNIaIaIaThrLeuTrpSerThrTrpLeuSerValPheYrCybVal 180  
18 ATAGGCAACCAACCAATGTATCAAGAACTATTAAAGAACATTTCAACCTTGAATGTC 540  
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24 GGAAGACACAGGAAGAGCTCTCTTACAACTCAGAGATTTCCAGAGGCCCACTGTGACG 720  
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RESULT 4
LOCUS CQ800046 957 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 50 from Patent WO2004029087.
ACCESSION CQ800046
VERSION CQ800046.1 GI:46848968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Bufer, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.
AUTHORS Bitter taste receptors
JOURNAL Patent: WO/2004029087-A 50 08-APR-2004;
DEUTSCHES INSTITUT FUER ERNAHRUNGSGESUNDH. (DE)
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ALIGNMENT Scores:
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Score: 1678.00 Matches: 318
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-628-464-2 (1-318) x CQ800046 (1-957)
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Qy 61 SerLeuGlyAlaSerArgPheCYsLeuGlnSerValValMetGlyYsThrIleTyrVal 80
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Db 481 ATNAGGACCAACGAAATGATACGAACTTTTAAGAACCACTTCAACCTTGGAAATGTC 540
Qy 181 ThrGlyAspSerIleArgSerTyrCYsGlyYsPheTyrLeuPheProLeuYsMetIle 200
Db 541 ACTGGGATAGCATACAGAGCTACTGTGAATTTCTATCTCTTCCCTTAATAATGATT 600
Qy 201 ThrTyrPheMetProThrAlaValPhePheIleCYsMetIleLeuLeuIleThrSerLeu 220
Db 601 ACTTGGACAAATGCCACTGCTGCTTTTTCATTTGATGATATTTTGTCTATCACTCTTG 660
Qy 221 GlyArgHisArgYsYsAlaLeuLeuThrThrThrSerGlyPheArgGlnProSerValGln 240
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Qy 241 AlaHisIleLeuAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260
Db 721 GCACACATTAAGGCTCTGCTGCTCTCTCTCTTTTGGCATGCTCTTCACTCATATTTTC 780
Qy 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheYsPheTTPVal 280
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Qy 281 TTPGLUserVal11eTyrLeuCYsAlaAlaValHisProIleIleLeuLeuPheSerAsn 300
Db 841 TGGAGTCACTGATTTATCTGTGTGTGCGAGCTTCACTTCACTTCTTCAAGCAG 900
Qy 301 CYsArgLeuAlaValLeuLeuYsSerArgSerSerArgCYsGlyThrPro 318
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RESULT 5
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DEFINITION Homo sapiens putative taste receptor T2R60 gene, complete cde.
ACCESSION AY114094
VERSION AY114094.1 GI:28603637
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barguin, P.J.
AUTHORS Identification and characterization of human taste receptor genes
JOURNAL belonging to the TAS2R family
MEDLINE Cytogenet. Genome Res. 98 (1), 45-53 (2002)
PUBMED 22471936
12584440
REFERENCE 2 (bases 1 to 957)
AUTHORS Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barguin, P.J.
JOURNAL Direct Submision
TITLE Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche
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Best Local Similarity:	100.00%
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DB:	9
Length:	957
Matches:	318
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-628-464-2 (1-318) X AY114094 (1-957)

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Qy	21	ValThrIleuLeuLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleThrAla	40
Db	61	GTTACCACTTTTACTCTTTTACCGCTGTGTAGCAATAGCAGGCATATGGCTTCACTGCT	12
Qy	41	AlaIleuGlyValGluTrpValIleuArgArgMetLeuLeuProCysAspIlyIleuLeuVal	60
Db	121	GCTCTGGCCGTGAGGGGTGCTACGAGAAATTTGTCCTTGATATGATATTTGTT	18
Qy	61	SeIeuGlyAlaSerArgPheCysIleuGlnSerValIValMetGlyPheThrIleTryVal	80
Db	181	AGCCTAGGGGCTCTCGCTTCTGTCTGCACTCACTGATAGGTATAGGATTAATTTATGT	24
Qy	81	PheIleuHisProMetAlaPheProTryAsnProValIleuGlnPheLeuAlaPheGlnTrp	10
Db	241	TTCTTGATCCGATGGGCTTCCATCAACCCGTACTCACTGATCACTTCTTCCAGTGG	30
Qy	101	AspPheLeuAsnAlaAlaThrIleuTrpSerSerThrTrpLeuSerAlaPheTryCysVal	12
Db	301	GACTCTCTGAATCTGCACCTTATGTCCTCTTCACTGGCTCAAGTCTCTTCAATGTGTG	36
Qy	121	IlyeIleAlaThrPheThrHisProValPhePheTrpLeuIlyHisIlyblyLeuSerGlyTrp	14
Db	361	AAATATGCTACTTTCACCCACCTGTCTTCTTGGCTTAAGCACAAGTTGCTGGGTGG	42
Qy	141	LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleuPhePhe	16
Db	421	CTACATGATGATGCTTCACTCTGTAGGGCTCTCCAGCTTCAACCATTTCTATTTTTC	48
Qy	161	IleGlyAsnHisArgMetTryGlnAsnTryLeuArgAsnHisIleuGlnProTrpAsnVal	18
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Qy	181	ThrGlyAspSerIleArgSerTryCysGluIlybPheTryLeuPheProLeuIlysmetIle	20
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Db	601	ACTTGGACATATGCCCATCTGCTGTTTTCATTGTGATGATTTTGTCTATCAATCTCG	66
Qy	221	GlyArgHisArgIlybIlyValaIleuLeuThrThnSerGlyPheArgGluProSerValGln	24
Db	661	GGAAGACACAGGAAGAAAGGCTTCTTACAACTCAGGATTCGGAAGGCCAGTGGCAG	72
Qy	241	AlaHisIleIlybAlaIleuLeuAlaIleuLeuSerPheAlaMetLeuPheIleSerTryPhe	26
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Qy	261	LeuSerIleuValPheSerAlaAlaGlyIlePheProProLeuAspPheIlybPheTrpVal	28
Db	781	CTGTCACTGTGTGTTACGTCTGCAGGATATTTTCCACTCTGGACTTTAAATTCGGGG	84
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Db 841 TGGAGTCAGTATTTATCTGTGTGACAGAGTTACACCCATTCATTCGCTTCAGCAAC 900

Qy 301 CyaArgLeuArgAlaValLeuIysSerArgArgSerSerArgCysGlyThrPro 318  
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901 TGCAGGCTAGAGCTGTGCTGAAGAGTGTCCTCAAGGTGTGGGACACCT 954

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LOCUS				
DEFINITION	Homo sapiens chromosome 7 taste receptor T2R56 gene, complete cds.			
ACCESSION	AY724955			
VERSION	AY724955.1	GI:51989208		

SOURCE ORGANISM	REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homini; Homidae; Homo.	2 (bases 1 to 957)
Anne, P., Yoav, G., Orna, M. and Svante, P.	Evolution of bitter taste receptors in human and apes
Unpublished	2 (bases 1 to 957)
Anne, P., Yoav, G., Orna, M. and Svante, P.	Direct Submission
Submitted (12-AUG-2004)	Genetics, Max-Planck Institute for
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany	

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ORIGIN		
Alignment Scores:		
Pred. No.:	5_41e-142	Length: 957
Score:	1678.00	Matches: 318
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
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JS-10-628-464-2 (1-318) x AY724955 (1-957)		

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Oy	21	ValIThrIleIleuDeuIleuAaArgIeuValAlaIlealagIyaNGlYPhelIethrAla	40
Db	61	GTTACATTTTACTCTTTTACGCTGGAGCAATAGCAGCAATGGCTTCATCATGCT	120
Oy	41	AlaIleuGlYValGluIThrValIleuAaArgIsmetIleuLeuProCYsaApyIleuIleuVal	60
Db	121	GCCTCTGGGGGTGAGGGGTGCTACAGGAATGTTGGTCCCTTGATGAAGTATTGGTT	180
Oy	61	SetIeuGlYAlaSerAaRphCYseuIInsSerValValIsmetGlYIytrmIleYVal	80
Db	181	AGCCTAGGGGGCCCTCTCGCTTCGTCTGCAGTCAGTCGAATGGGTAAAGACATTATAGTT	240
Oy	81	PhleuIHisIerProMetAlaPheProTYaenProValIleuGlnIleuAlaIaPheGlnITrp	100





QY 161 ILGLYASNHISARGMETYRGINAERTYRLAUAARGASNHISLEUGINPROTPAENVAL 180  
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DB 63357 ACTGGGCAATGACATACGAGACTACTGTGAGAAATTCATCTCTCCCTTAATAAATGATT 63416  
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ACCESSION AY724901  
VERSION AY724901.1 GI:51989117  
KEYWORDS Pan troglodytes (chimpanzee)  
SOURCE Pan troglodytes  
ORGANISM  
REFERENCE  
AUTHORS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
TITLE 1 (bases 1 to 957)  
JOURNAL Anne, F., Yeay, G., Orna, M. and Svante, P.  
REFERENCE Evolution of bitter taste receptors in human and apes  
AUTHORS 2 (bases 1 to 957)  
TITLE Unpublished  
JOURNAL  
REFERENCE Direct Submission  
AUTHORS Submitted (12-AUG-2004) Genetec, Max-Planck Institute for  
JOURNAL Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany  
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QY 61 SerleuGlyAlaSerArgPheCyseleuGlnSerValValMetGlyLysThrIleTyRval 80  
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AY724866  
VERSION  
AY724866.1 GI:51989057  
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SOURCE  
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
REFERENCE  
1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes  
TITLE  
Unpublished  
2 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Direct Submission  
AUTHORS  
Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
JOURNAL  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany  
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DB 121 GCTCTGGCGGTGGAGTGGCTCTACGAGAAATGTTGCTTGTGATTAATTTGGTT 180  
QY 61 SerleuglyAlaseraPheCyaleuglinservAlaValmetGlylythrileTyVal 80  
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DB 901 TGCAGGCTGAGACCTGCTGTAAGAGTCCGCTTCTCAAGGTGTGGACACCT 954  
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LOCUS Gorilla gorilla chromosome 7 taste receptor T2R56 gene, complete  
DEFINITION  
AY724923  
VERSION  
AY724923.1 GI:51989154  
KEYWORDS  
SOURCE  
ORGANISM  
Gorilla gorilla (gorilla)  
Gorilla gorilla  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.  
REFERENCE  
1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes  
TITLE  
Unpublished  
2 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Direct Submission  
AUTHORS  
Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
JOURNAL  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany  
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KEWVESVIYLCAAVHPILLFNSNRLRAVLKSCRSSRCTP"

## ALIGNMENT SCORES:

Pred. No.:	6.06e-137	Length:	957
Score:	1622.00	Matches:	307
Percent Similarity:	97.80%	Conservative:	4
Best Local Similarity:	96.54%	Mismatches:	7
Query Match:	96.66%	Indels:	0
DB:	9	Gaps:	0

US-10-628-464-2 (1-318) x AY724986 (1-957)

QY 1 MetAaNGIYAAsphIsmetValleuGIySerSerValThraSphlyblyAlaileleu 20  
DB 1 ATGAATGAGACCAACATGTTCTAGATCTTCGGTACTACAGAGGCCATCATCTTG 60  
QY 21 ValThrIleuLeuLeuLeuAurgleuValAlaileuAGIYAAsngIyPheileThra 40  
DB 61 GTTACCATTTTACTCTCTTTTACCGCTGTGACATAGCAGCATGGCTTCATCTGCT 120  
QY 41 AlaleuGIyValIuTrpValleuAurgleuMetleuLeuProCybaSphlyblyleuVal 60  
DB 121 GCTCTGGCGGTGAGTGGGTGCTACAGAGATGTGTGCTTGTGATGATGATGATG 180  
QY 61 SerleuGIyAlaSerArPheCySleuGIySerValValmetGIyThrIleYVal 80  
DB 181 AGCTAGGGGCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 81 PheleuHiaProMetAlaPheProTyYAsnProValleuGIyPheleuAlaPheGIyTrp 100  
DB 241 TTCTTCATCCGATGCGCTTCCCATACACCTGTACTGACATTTTCCAGTGG 300  
QY 101 AAspPheleuAAsnAlaIaThrIleuTrpSerSerThrTrpLeuSerValPheTyYCyVal 120  
DB 301 GACTTCTGATGATGCTGACCTTATGTTCTTCACTGCGCTCAGTGTCTTATTTG 360  
QY 121 LysIleAlaThrPheThrIaSProValPhePheTrpLeuYshIySlyleuSerGIyTrp 140  
DB 361 AAAATTCGCTCTTTCACCCACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 141 LeuProTrpMetleuPheSerSerValGIyLeuSerSerPheThrIleuPhePhe 160  
DB 421 CTACCATGATCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 161 IleGIyAAsnHiaPheMetTyYArgIaenTyYleuAurgleuHiaSleuGIyProTrpAenVal 180  
DB 481 ATAGGCAACCAACGAAATGATACGAACTACTTAAAGAAACATCTTACCACTTGAATATC 540  
QY 181 ThrGIyAspSerIleArSerTyYCySGLySlyPheTyYleuPheProleuYsmetIle 200  
DB 541 ACTGCAATGATGATGAGGCTACTGAGAAATTTCTATCTTCCCTCTTAAAAATGATT 600  
QY 201 ThrTrpThrMetProThraIaValPhePheIleCySmetIleleuLeuIleThrSerleu 220  
DB 601 ACTTGGACATGCGCCACGCTGCTTCTTTCATTTGCTGCTGCTGCTGCTGCTGCTG 660  
QY 221 GIYArgHiaArgIySlyblyAlaileuLeuThrThraSerGIyPheArgIuProSerValGIu 240  
DB 661 GGAAGACACATGAGAGGCTCTCTTAAACCTCAGGATTCGAGAGGCCAATATGACAG 720  
QY 241 AlaHiaIleYblyAlaileuLeuAlaileuLeuSerPheAlaMetleuPheIleSerTyYPhe 260  
DB 721 GCACACATTAAGGCTGCTGCTGCTCTCTCTTTCGCTGCTGCTTCACTCATATTTTC 780  
QY 261 LeuSerleuValPheSerAlaIaIaGIyIlePheProProleuAAspPheTyYblyTrpVal 280

DB 781 CTGTCACTGATGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 281 TrpGIySerValIleYblyleuCySAlaIaValHiaProIleleuLeuPheSerAen 300  
DB 841 TGGAACTCAGTATTTATCTGTTGAGCGGTTCACCCATCATTTGCTCTTCAGCAAC 900  
QY 301 CySArGIyAlaIaIaIleuYblySerArGIySerSerArGIyCySGLyThraPro 318  
DB 901 TGCAGGCTAGAGCTGTGCTGAGAGATTGCCGTTCTCTCAAGGTGTGAGACACT 954

## RESULT 11

AY724986 957 bp DNA linear PRI 18-SEP-2004  
LOCUS Pongo pygmaeus chromosome 7 taste receptor T2R56 gene, complete  
DEFINITION cds  
VERSION AY724986  
KEYWORDS AY724986.1 GI:51989260  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus

REFERENCE  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Direct Substitution  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES  
source Location/Qualifiers

## CDS

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## ORIGIN

## ALIGNMENT SCORES:

Pred. No.:	3.31e-127	Length:	957
Score:	1514.00	Matches:	289
Percent Similarity:	94.65%	Conservative:	12
Best Local Similarity:	90.88%	Mismatches:	17
Query Match:	90.23%	Indels:	0
DB:	9	Gaps:	0

US-10-628-464-2 (1-318) x AY724986 (1-957)

QY 1 MetAaNGIYAAsphIsmetValleuGIySerSerValThraSphlyblyAlaileleu 20  
DB 1 ATGAATGAGACCAACATGTTCTAGATCTTCGGTACTACAGAGGCCATCATCTTG 60  
QY 21 ValThrIleuLeuLeuLeuAurgleuValAlaileuAGIYAAsngIyPheileThra 40  
DB 61 GTTACCATTTTACTCTCTTTTACCGCTGTGACATAGCAGCATGGCTTCATCTGCT 120  
QY 41 AlaleuGIyValIuTrpValleuAurgleuMetleuLeuProCybaSphlyblyleuVal 60  
DB 121 GCTCTGGCGGTGAGTGGGTGCTACAGAGATGTGTGCTTGTGATGATGATGATG 180



QY 61 SerLeuG1ValAspSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
 DB 181 AGCTTAGGGGCTCTGCTCTTTTGTCTCACTGGGGTGAATGGTAAGACCACTTAATGTT 240  
 QY 81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTyr 100  
 DB 241 TTCTTGATCCGACGGCTTCCCATACACCTGTACTGGGGTTTCTAGCTTCCAGTGG 300  
 QY 101 AspPheLeuAsnAlaAlaThrLeuTyrSerSerThrTyrLeuSerValPheTyrCysVal 120  
 DB 301 GACTTGCTGAATGCTGACCTTAATGTTCTCTACCGGCTTACGTCTTCTATATGTTG 360  
 QY 121 LysIleAlaThrPheThrHisProValPhePheThrLeuLysHisLysLeuSerGlyTyr 140  
 DB 361 AAAATTCCTACCTTACCCACCTCTCTCTCTCTGCTTAAGACACAAAGTTGCTGAGTGG 420  
 QY 141 LeuProTyrMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160  
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 DB 481 ATAGGCAACCATAGATATATACAGACCTATTAAAGAACCATCTACCACTTGAATGTC 540  
 QY 181 ThrGlyAspSerIleArgSerTyrCysGlyLysPheTyrLeuPheProLeuLysMetIle 200  
 DB 541 ACTGGCAATGACATATGAGCTACTGTAGAAATTTCTACTCTTCCCTCTAAATAATATTT 600  
 QY 201 ThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
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 QY 221 GlyArgHisArgLysValAlaLeuLeuThrThrSerGlyPheArgLysProSerValGln 240  
 DB 661 GGAAGACACATGAAGAAGGCTCTCTCTTAACAACCTCAGATTTCCAGAGCCACAGTGTG 720  
 QY 241 AlaHisIleLysValAlaLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
 DB 721 GCACACATTAAGGCTATGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 QY 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheLysPheTyrVal 280  
 DB 781 CTGTCACTGGTGTTCATGCTGCTGAGGATTTTTCACCTCTGACCTTAAATTCGTGGTG 840  
 QY 281 TyrGlnSerValIleTyrLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
 DB 841 TGGGAGTCAGTGAATTTATCTGTGTGTCAGCAGCTTCACTCATCTTCTCAGCAAC 900  
 QY 301 CysArgLeuArgAlaValLeuLysSerArgArgSerSerArgCysGlyThrPro 318  
 DB 901 CGCAGGCTGAGAGCTGTGCTGAAGAGTGCCTGCTCAAGGTGTGGACACCT 954

RESULT 12  
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 LOCUS Macaca mulatta chromosome 7 taste receptor T2R56 gene, complete  
 DEFINITION  
 c8.  
 ACCESSION AY725022  
 VERSION AY725022.1 GI:51989321  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Macaca mulatta (rhesus monkey)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecidae; Macaca.  
 1 (bases 1 to 957)  
 Anne F., Yoav G., Orna M. and Svante P.  
 Evolution of bitter taste receptors in human and apes  
 JOURNAL  
 Unpublished  
 2 (bases 1 to 957)  
 Anne F., Yoav G., Orna M. and Svante P.  
 TITLE  
 Direct Submission

JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
 Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
 Germany

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 SLGRHMEKALITTSGRFSPVQAHVALALSLAMLFISYFLSLVLSAAGIPPLPDE  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.85e-124 Length: 957  
 Score: 1480.00 Matches: 285  
 Percent Similarity: 92.77% Conservative: 10  
 Best Local Similarity: 89.62% Mismatches: 23  
 Query Match: 88.20% Indels: 0  
 DB: 9 Gaps: 0

US-10-628-464-2 (1-318) x AY725022 (1-957)

QY 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspLysAlaIleIleLeu 20  
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 QY 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40  
 DB 61 GTTATCATTTTACTCTTTTGTGCTGCTGTGACATAGCAGGCAATGGCTTCACTGCT 120  
 QY 41 AlaLeuGlyValGlnTyrValLeuArgArgMetLeuLeuProCysAspLysLeuLeuVal 60  
 DB 121 GCTGGGTGTGGAGTGGGTGTACAGGGGAACCTGTGTGCTGTGATAGTAACTGCTT 180  
 QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
 DB 181 AGCTTAAGGGCTCTGCTCTTTTGTCTGCACTGGGTGTATAGGTGAACCATTTATGTT 240  
 QY 81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTyr 100  
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 QY 101 AspPheLeuAsnAlaAlaThrLeuTyrSerSerThrTyrLeuSerValPheTyrCysVal 120  
 DB 301 GACTTGCTGAATGCTGACCTTAATGTTCTCTACCGGCTTACGTCTTCTATATGTTG 360  
 QY 121 LysIleAlaThrPheThrHisProValPhePheThrLeuLysHisLysLeuSerGlyTyr 140  
 DB 361 AAAATTCCTACCTTACCCACCTCTCTCTCTCTGCTTAAGACACAAAGTTGCTGAGTGG 420  
 QY 141 LeuProTyrMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160  
 DB 421 GTACCGTGATGCTCTTCACTGCTGTAGGGCTTCCAGCTTCCACCACTTCTATTTTTC 480  
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 DB 481 ATAGGCAACCATAGATATATACAGACCTATTAAAGAACCATCTACCACTTGAATGTC 540  
 QY 181 ThrGlyAspSerIleArgSerTyrCysGlyLysPheTyrLeuPheProLeuLysMetIle 200  
 DB 541 ACTGGCAATGACATATGAGCTACTGTAGAAATTTCTACTCTTCCCTCTAAATAATATTT 600  
 QY 201 ThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: February 4, 2005, 18:42:27 ; Search time 617 Seconds

(without alignments)  
3051.017 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678  
Sequence: 1 NMGDHVAVLSSVTDKKAIL.....SNCRLAVALKRRSRRCGRP 318

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US10628464/runcat.04022005\_115947\_4317/app\_query.fasta\_1.455  
-DB=N\_Geneseq.16Dec04 -OPMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	954	6	ABK87584 DNA encod
2	1678	100.0	957	12	ADJ87104 Nucleotid
3	1678	100.0	957	13	ADM33336 Human bit
4	960	57.2	939	8	ACC44449 Gene enco
5	609	36.3	924	6	AAS18172 Human T2R

6	609	36.3	924	6	AB243209	Ab243209 Human GPC
7	609	36.3	924	13	ADR29249	ADR29249 Taste rec
8	609	36.3	1324	10	ADC68988	ADC68988 Human GPC
9	608	36.2	921	13	ADM33294	ADM33294 Human bit
10	600.5	35.8	9437	5	AAF92567	AAF92567 Mouse T2R
11	600.5	35.8	9437	13	ADR29217	ADR29217 Taste rec
12	593.5	35.4	1295	5	AAF92539	AAF92539 Rat T2R12
13	593.5	35.4	1295	13	ADR29161	ADR29161 Taste rec
14	425	25.3	885	8	ACC44453	ACC44453 Gene enco
15	416	24.8	873	13	ADM33330	ADM33330 Human bit
16	409	24.4	897	8	ACC44450	ACC44450 Gene enco
17	408	24.3	876	5	AAF92516	AAF92516 Human T2R
18	408	24.3	876	12	ADJ84512	ADJ84512 Human T2R
19	408	24.3	876	13	ADR29092	ADR29092 Taste rec
20	402.5	24.0	882	8	ACC44448	ACC44448 Gene enco
21	380	22.6	2887	5	AAF92559	AAF92559 Mouse T2R
22	380	22.6	2887	13	ADR29201	ADR29201 Taste rec
23	378.5	22.6	954	12	ADJ84495	ADJ84495 Human T2R
24	378.5	22.6	954	13	ADM33318	ADM33318 Human bit
25	378.5	22.6	957	12	ADQ17198	ADQ17198 Human bof
26	378.5	22.6	957	12	ADQ21802	ADQ21802 Human bof
27	378.5	22.6	957	12	ADQ17321	ADQ17321 Human bof
28	378.5	22.6	957	13	ADR29075	ADR29075 Taste rec
29	375.5	22.4	957	5	AAF92508	AAF92508 Human T2R
30	359	21.4	936	13	ADM33322	ADM33322 Human bit
31	359	21.4	939	5	AAF92510	AAF92510 Human T2R
32	359	21.4	939	12	ADJ84499	ADJ84499 Human T2R
33	359	21.4	939	13	ADR29079	ADR29079 Taste rec
34	356	21.2	914	12	ADJ84453	ADJ84453 Rat T2R G
35	356	21.2	6552	5	AAF92530	AAF92530 Rat T2R03
36	356	21.2	6552	13	ADR29143	ADR29143 Taste rec
37	345.5	20.6	939	8	ACC44451	ACC44451 Gene enco
38	344.5	20.5	1304	5	AAF92533	AAF92533 Rat T2R06
39	344.5	20.5	1304	13	ADR29149	ADR29149 Taste rec
40	341.5	20.4	957	12	ADQ22066	ADQ22066 Human bof
41	339	20.2	966	6	AAS18165	AAS18165 Human T2R
42	339	20.2	966	13	ADR29235	ADR29235 Taste rec
43	339	20.2	1017	6	AB243207	AB243207 Human GPC
44	339	20.2	1366	10	ADC87278	ADC87278 Human GPC
45	339	20.2	1417	10	ADC87332	ADC87332 Human GPC

#### ALIGNMENTS

RESULT 1	ABK87584	standard; cDNA; 954 BP.
ID	ABK87584	
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AC	ABK87584;	
DT	24-SEP-2002	(first entry)
XX		
DE	DNA encoding novel human G-protein coupled receptor.	
XX		
KW	G-protein coupled; receptor; liver; central nervous system disease;	
KW	Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;	
KW	hyperlipemia; cancer; non-small cell lung cancer; ovarian cancer;	
KW	stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;	
KW	circulatory disease; hypertension; atherosclerosis; angina; allergy;	
KW	inflammatory disease; respiratory disease; asthma; bronchitis;	
KW	digestive disease; stomach ulcer; duodenal ulcer; immune disorder;	
KW	autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;	
KW	pneumonia; influenza; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..954
FT		/tag= a
FT		/product= "Novel G-protein coupled receptor"
FT		/partial
XX		/note= "No stop codon given"



XX WPI: 2004-143845/14.  
 DR P-PSDB; ADJ87105.  
 XX Novel isolated bitter taste receptor, T2R76 polypeptide useful for  
 PT identifying modulators of taste perception, or bitter compounds.  
 XX  
 PS Claim 1, Page 97-98; 100pp; English.  
 XX  
 CC The present sequence encodes human bitter taste receptor T2R76. The human  
 CC T2R76 gene is located on chromosome 7 in the region 14q62692-14q63448.  
 CC The reading frame of T2R76 is intronless. T2R76 polypeptides and  
 CC polynucleotides are useful for identifying modulators. Such modulators  
 CC are useful for modulating bitter taste perception in a subject. T2R76  
 CC agonists can be administered to enhance bitter tastes, while T2R76  
 CC antagonists can be administered to reduce bitter taste.  
 XX  
 SQ Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,05e-160 Length: 957  
 Score: 1678.00 Matches: 318  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0  
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 QY 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspLysAlaIleLeu 20  
 DB 1 ATGATGAGACCAACAGTTCCTAGATCTTCGGTGAAGCAAGAGCCATATCTTG 60  
 QY 21 ValThrIleuLeuLeuLeuLeuValAlaIleAglYasnGlyPheIleThAla 40  
 DB 61 GTTACCATTTTACTCTTTTACGGCTGTGACATACAGGCAATGCTTCATCATGCT 120  
 QY 41 AlAlenGlyValAluTTPValLeuArgMetLeuLeuProCysAspLysLeuVal 60  
 DB 121 GCTTGCGCGGTGGAGTGGGTCTAGAGAAATGTTGCTGTGTGAATGATATGCTT 180  
 QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
 DB 181 AGCTTAGGGGCTCTCGCTTCTGTCTGACAGTGTAAAGGTAAGACATTATGTT 240  
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 DB 241 TTCTTCATCCGATGGAGGCTTCCCATACACCTGTACTGAGTTCTTAGCTTCCAGTGG 300  
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 QY 241 AlHisIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
 DB 721 GCACACATAAAGGCTGCTGCTCTCTCTCTTTTGCATGCTTCATCATATATTC 780  
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 QY 281 TyrGlySerValIleTyrLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
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 ID ADM33336  
 XX ADM33336;  
 AC ADM33336;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.  
 XX  
 KM human; bitter taste receptor; food; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT CDS 1..957  
 FT /product= "bitter taste receptor hTAS2R60"  
 FT  
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 FN W02004029087-A2.  
 XX  
 XX 08-APR-2004.  
 PD  
 XX 25-SEP-2003; 2003WO-EP010691.  
 PF  
 XX 25-SEP-2002; 2002US-0413298P.  
 PR  
 XX (DEER-) DEUT INST ERNAHRUNGSFORSCHUNG POTSDAM.  
 PA  
 XX Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
 PI WPI: 2004-305149/28.  
 DR P-PSDB; ADM33335.  
 DR  
 XX Novel bitter receptor polynucleotide encoding human TAS2R protein having  
 PT bitter substance binding activity, useful for producing nutraceutical or  
 PT pharmaceutical compositions comprising antagonists of bitter taste  
 PT receptor activity.  
 PT  
 XX  
 XX Claim 14; SEQ ID NO 50; 108pp; English.  
 XX  
 CC The present sequence encodes a human bitter taste receptor. Also  
 CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
 CC a vector (II) containing (I); (3) a host cell (III) genetically  
 CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
 CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
 CC acid sequence encoded by (I) or obtained by culturing (III) and  
 CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
 CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
 CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
 CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
 CC isolating (M1) a compound that binds to (V) encoded by (I); (10)  
 CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a



Score:	960.00	Matches:	183
Percent Similarity:	73.70%	Conservative:	46
Best Local Similarity:	58.77%	Mismatches:	81
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US-10-628-464-2 (1-318) X ACC44449 (1-939)

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Qy	121 Lye1leAla1a8rPheThrla8rProVa1PheRheTrbLeu1a8rVbLeuSeRg1yTr	140
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XX	26-MAR-2002	(first entry)	
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KW	taste transduction; food taste masking; drug taste masking.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
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PN	WO200177676-A1.		
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PD	18-OCT-2001.		
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PE	04-APR-2001; 2001MO-US010739.		
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PR	07-APR-2000; 2000US-0195532P.		
PR	13-NOV-2000; 2000US-0247014P.		
XX			
PA	(SENO-) SENOMYX INC.		
XX			
PI	Adler JE;		
XX			
DR	WPI; 2002-017486/02.		
DR	P-PsDB; AAU11389.		
XX			
PT	Novel isolated mammalian taste cell-specific G protein-coupled receptor,		
PT	T2R, involved in bitter taste sensation, useful for identifying taste		
PT	modulators that are used to decrease or mask bitter taste of foods or		
PT	drugs.		
PS	Claim 1; Page 74; 103pp; English.		
XX			
CC	The invention relates to a mammalian taste cell-specific G protein-		
CC	-coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste		
CC	sensation. The T2R polypeptides and their associated polymucleotides are		
CC	useful for screening one or more compounds for the presence of taste		
CC	detectable by a mammal. Modulators of T2R polypeptides (modulators of		
CC	taste transduction) are useful for pharmacological and genetic		
CC	modulations of taste signalling pathways. These modulatory compounds are		
CC	then used in food and pharmaceutical industries to customise taste, e.g.,		
CC	to decrease or mask the bitter taste of foods or drugs. This sequence		
CC	represents cDNA encoding the human T2R71 (ht2r71) polypeptide		
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DT	26-MAR-2002	(first entry)	
XX			
DE	Human T2R71 (ht2r71)	CDNA..	
XX			
KW	Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor; ht2r71; T2R71; T2R; bitter taste sensation; taste signalling pathway; ss		
KW	taste transduction; food taste masking; drug taste masking.		
XX			
OS	Homo sapiens.		
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PR	13-NOV-2000; 2000US-0247014P.		
XX			
PA	(SENO-) SENOMYX INC.		
XX			
PI	Adler JE;		
XX			
DR	WPI; 2002-017486/02.		
XX			
DR	P-PADB; AAU11389.		
XX			
PT	Novel isolated mammalian taste cell-specific G protein-coupled receptor,		
PT	T2R, involved in bitter taste sensation, useful for identifying taste		
PT	modulators that are used to decrease or mask bitter taste of foods or		
PT	drugs.		
PS	Claim 1; Page 74; 103pp; English.		
XX			
CC	The invention relates to a mammalian taste cell-specific G protein-		
CC	-coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste		
CC	sensation. The T2R polypeptides and their associated polymucleotides are		
CC	useful for screening one or more compounds for the presence of taste		
CC	detectable by a mammal. Modulators of T2R polypeptides (modulators of		
CC	taste transduction) are useful for pharmacological and genetic		
CC	modulations of taste signalling pathways. These modulatory compounds are		
CC	then used in food and pharmaceutical industries to customise taste, e.g.,		
CC	to decrease or mask the bitter taste of foods or drugs. This sequence		
CC	represents cDNA encoding the human T2R71 (ht2r71) polypeptide		
SQ	Sequence 924 BP; 180 A; 249 C; 214 G; 281 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	4,76e-52	Length:	924
Score:	609.00	Matches:	122
Percent Similarity:	57.73%	Conservative:	46
Best Local Similarity:	41.92%	Mismatches:	111
Query Match:	36.29%	Indels:	12
DB:	6	Gaps:	2
US-10-628-464-2 (1-318) x AAS18172 (1-924)			
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Db	28 GTGTGGTCTTTAGCCTCGCTGAGTCCTTCGGGGATTGGAGGAATGGCTTCATTGTGCTG 87		
OY	41 AlAleNGlyValGluTrpValLeuArgAmgMetLeuLeuProCyAspLyLeuLeuVal 60		
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DB 268 CACTTCTTAACCTACACACCTCTTCTGTTTGGACGTGGCTCAAGTCTCTGTTCTGTGG 327
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OY 236 GluProSerValGlnIleHisIleValAlaLeuLeuAlaLeuLeuSerPheAlaMetLeu 255
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XX 06-MAR-2003 (first entry)
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XX KM Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
XX drug development; gustatory; taste; fragrance; gene; de.
XX OS Homo sapiens.
XX PN MO200216548-A2.
XX PD 28-FEB-2002.
XX PF 30-JUL-2001; 2001WO-1B001446.
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XX 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Haga T, Takeda S, Mitaku S;
PI WPI; 2002-304118/34.
DR P-PDB; ABP95935.
XX Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
PS Claim 9; SEQ ID NO 679; 97pp + Sequence Listing; Japanese.
XX The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP9596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 924 BP; 180 A; 249 C; 214 G; 281 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4,766-52 Length: 924
Score: 609.00 Matches: 122
Percent Similarity: 57.73% Conservative: 46
Best Local Similarity: 41.92% Mismatches: 111
Query Match: 36.29% Indels: 12
DB: Gaps: 2
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OY 81 PheLeuNIAPrometalApeProTyrAanProValIleuGlnPheLeuAlaPheGlnTyr 100
DB 208 TCTGCCACAGAGTCACTCTGGGGGCTCTCGGCCGACAGTCTTCCATCTACACTGG 267
OY 101 AspPheLeuAsnAlaIalAthrLeuTyrPseSerSerThrTyrLeuSerValIleTyrCysVal 120
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DB 388 GTGCGCTGGCTCTGTTGGGCTCTGCTGCTGATCTCTTCATCAATACCTCGTGTCTTTT 447
OY 161 IleGlyAsnHisArgMetTyrGlnAanTyrLeu-----ArgAsnHisLeu 175
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6	378.5	22.6	954	4 US-09-393-634-48	Sequence 48, Appl
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8	378.5	22.6	4957	4 US-09-949-016-15124	Sequence 15124, A
9	359	21.4	939	4 US-09-393-634-52	Sequence 52, Appl
10	358	21.3	12226	4 US-09-949-016-12237	Sequence 12237, A
11	356	21.2	1463	4 US-09-393-634-6	Sequence 6, Appl
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18	319.5	19.0	1331	4 US-09-393-634-2	Sequence 2, Appl
19	304	18.1	912	4 US-09-393-634-59	Sequence 59, Appl
20	293	17.5	900	4 US-09-393-634-44	Sequence 44, Appl
21	293	17.5	900	4 US-09-949-016-1071	Sequence 1071, Ap
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26	280	16.7	250352	4 US-09-949-016-14724	Sequence 14724, A
27	279	16.6	1084	4 US-09-393-634-20	Sequence 20, Appl
28	273.5	16.3	924	4 US-09-393-634-54	Sequence 54, Appl
29	270	16.1	1540	4 US-09-393-634-8	Sequence 8, Appl
30	266.5	15.9	900	4 US-09-393-634-42	Sequence 42, Appl
31	254	15.1	903	4 US-09-393-634-63	Sequence 63, Appl
32	240.5	14.3	2438	4 US-09-393-634-63	Sequence 63, Appl
33	231.5	13.8	954	4 US-09-393-634-4	Sequence 4, Appl
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35	212.5	12.7	1739	4 US-09-393-634-16	Sequence 16, Appl
36	203.5	12.1	819	4 US-09-393-634-10	Sequence 10, Appl
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39	196.5	11.7	601	4 US-09-949-016-108296	Sequence 108296, A
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41	177.5	10.6	601	4 US-09-949-016-38510	Sequence 38510, A
42	177.5	10.6	601	4 US-09-949-016-80952	Sequence 80952, A
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44	169	10.1	601	4 US-09-949-016-38861	Sequence 38861, A
45	169	10.1	601	4 US-09-949-016-78195	Sequence 78195, A

#### ALIGNMENTS

RESULT 1  
US-09-949-016-12790  
; Sequence 12790, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTNER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: Q1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 12790  
; LENGTH: 4876  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12790

Alignment Scores:  
Pred. No.: 1.03e-39  
Score: 418.50  
Percent Similarity: 48.47%  
Best local Similarity: 30.06%  
Query Match: 24.94%  
DB: 4  
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US-10-628-464-2 (1-318) x US-09-949-016-12790 (1-4876)  
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RESULT 2  
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 ; Sequence 14084, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 14084
; LENGTH: 4877
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14084

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## Alignment Scores:

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Pred. No.: 1,03e-39 Length: 4877
Score: 418.50 Matches: 98
Percent Similarity: 48.47% Conservative: 60
Best Local Similarity: 30.06% Mismatches: 141
Query Match: 24.94% Indels: 27
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US-10-628-464-2 (1-318) x US-09-949-016-14084 (1-4877)

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GenCore version 5.1.6  
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Run on: February 4, 2005, 21:46:44 ; Search time 618 Seconds

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Total number of hits satisfying chosen parameters: 8627612

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	609	36.3	924	9 US-09-825-882-17	Sequence 17, Appl1
3	609	36.3	924	17 US-10-343-650A-679	Sequence 679, Appl
4	609	36.3	924	18 US-10-724-208-17	Sequence 17, Appl
5	609	36.3	924	18 US-10-724-208-17	Sequence 18, Appl
6	609	36.3	924	18 US-10-724-208-17	Sequence 17, Appl
7	609	36.3	924	18 US-10-724-208-17	Sequence 17, Appl
8	609	36.3	924	18 US-10-724-208-17	Sequence 17, Appl
9	600.5	35.8	924	17 US-10-017-161-1785	Sequence 1441, Ap
10	600.5	35.8	924	17 US-10-292-798-1441	Sequence 1441, Ap
11	593.5	35.4	924	17 US-10-724-208-17	Sequence 156, App
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13	408	24.3	876	9 US-09-510-332-156	Sequence 100, App
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24	378.5	22.6	954	9 US-09-393-634-65	Sequence 65, Appl
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43	339	20.2	966	18 US-10-723-860-148	Sequence 88, Appl
44	339	20.2	966	18 US-10-723-860-148	Sequence 88, Appl
45	339	20.2	1017	17 US-10-343-650A-675	Sequence 675, App

#### ALIGNMENTS

RESULT 1  
US-10-628-464-1  
Sequence 1, Application US/10628464  
Publication No. US2004012134A1  
GENERAL INFORMATION:  
APPLICANT: ADLER, JON ELLIOT  
APPLICANT: TANG, HUIXIAN  
APPLICANT: PRONIN, ALEKSEY  
TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
FILE REFERENCE: 10037, 54260US  
CURRENT FILING DATE: 2003-07-29  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 1  
LENGTH: 957  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

LOCATION: (1) . (954)  
US-10-628-464-1

## Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
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US-10-628-464-2 (1-318) x US-10-628-464-1 (1-957)

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Db 241 TTCTTGATCCGATGGGCTTCCCATACMACCTGTACTGAGTTCAGTTCCTTCCAGTGG 300
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## RESULT 2

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; Sequence 17, Application US/09825882
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; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-882-17
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QY 21 ValThrIleLeuLeuLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40
Db 28 GTTTCCTTTAGCTGTGATGCTTCTGGGATTTGACGCAATGGCTTCAATGTCGTG 87
QY 41 AlaLeuGlyValGlnTrpValLeuArgArgMetLeuLeuProCysAspLysLeuVal 60
Db 88 GTGCTGGGAGGAGGTGCGATATGCAAGTGTGCTCCCTTGATGTGATCCCAT 147
QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyVal 80
Db 148 AGCTTGGGTGCTCCGCTTGTGCTGCAAGTGTGGACGAGTGCACAACTTTCATC 207
QY 81 PheLeuHisProMetAlaPheProTyArgAspProValLeuGlnPheLeuAlaPheGlnTrp 100
Db 208 TGTGCCAGAAAGTGAATGATCTGGGGGTCTCGGCCGACAGTTCATCATACACTGG 267
QY 101 AspPheLeuAsnAlaAlaThrLeuTrpSerSerThrTrpLeuSerValPheTyArgVal 120
Db 268 CACTTCCTGATCACTCACCACTTGTGTTTGCAGCTGGCTCAAGTCTGTCTGTGTG 327
QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuLysHisLysLeuSerGlyTrp 140
Db 328 AGATTTGCTAAATCATCACACTCCACTTCTGTGCTGATAGTGAAGTCCAGAGTGG 387
QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhe 160
Db 388 GTGCCCTGGCTGTGTGGGCTGTGCTGATCTCTTCATCATTAACCTGCGTGTGTTT 447
QY 161 IleGlyAsnHisArgMetTyArgLysLeuLeu-----ArgAsnHisLeu 175
Db 448 TGGGTGAACCTACCTGTATATCAAGAAATTTTAAGAAAATTTTCTGGAAACATGACC 507
QY 176 GlnProTrpAsnValThrGlyAspSerIleArgSerTyArgGlyLysPheTyLeuPhe 195
Db 508 TACAACTGGAAT-----ACAAAGATGAAACATACATATTTTCCCA 546
QY 196 ProLeuLysMetIleThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeu 215
```

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: February 4, 2005, 19:59:28 ; Search time 3688 Seconds

(without alignments)  
3282.114 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678  
Sequence: 1 MNDGHWLVGSSVTDKXAIL.....SNCRLRAVLKRRSSRCGP 318

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ .p2n.model -DEV=xlh  
-O=/cgr2.1/USPTO.spool/US10628464/runat\_04022005\_115948\_4337/app.query.fasta\_1.455  
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pic -NOR=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US10628464.OCGN\_1\_1\_4352.0/runat\_04022005\_115948\_4337 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: +  
1: gb\_est1: +  
2: gb\_est2: +  
3: gb\_hic: +  
4: gb\_est3: +  
5: gb\_est4: +  
6: gb\_est5: +  
7: gb\_est6: +  
8: gb\_gss1: +  
9: gb\_gss2: +

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	20.6	893	9	AY403663 Pan trogl
2	336	20.0	900	9	AY403662 Homo sapi
3	326	19.4	894	9	AY403664 Mus muscu
4	321.5	19.2	866	7	CN840760 AGENCOURT
5	307.5	18.3	717	7	CF147792 AGENCOURT
6	297.5	17.7	771	9	CC544773 CH240_427
7	293	17.5	806	4	BG209561 RST29087
8	286.5	17.1	895	7	CN839536 AGENCOURT
9	284	16.9	650	8	AQ316999 CITR1-E1-

10	284	16.9	742	8	AQ308694
C 11	284	16.9	787	8	AZ739176
C 12	283	16.9	850	7	CN835406
C 13	262	15.6	917	7	CN842886
C 14	254.5	15.2	851	9	CC521365
C 15	246.5	14.7	883	7	CN836429
C 16	245.5	14.6	894	9	AY404528
C 17	235	14.0	715	7	CF147795
C 18	234	13.9	700	8	BH265706
C 19	232	13.8	530	9	CE673154
C 20	232	13.8	913	7	CN843081
C 21	228	13.5	2418	3	AF116728
C 22	227	13.5	493	8	B2898478
C 23	221.5	13.2	870	9	CR071716
C 24	214	12.8	718	7	CF147794
C 25	211.5	12.6	884	7	CN839562
C 26	210	12.5	921	7	CN843110
C 27	207	12.3	758	4	BG203110
C 28	207	12.3	853	7	CN839414
C 29	206.5	12.3	921	7	CN835918
C 30	204.5	12.2	744	7	CO935442
C 31	204	12.2	737	7	CO960534
C 32	201.5	12.0	639	8	B2922748
C 33	199.5	11.9	852	7	CN835976
C 34	198.5	11.8	900	9	AY404526
C 35	196	11.7	414	8	BH614820
C 36	193	11.5	741	9	AG374557
C 37	191.5	11.4	871	7	CN835432
C 38	191	11.4	711	7	CF147793
C 39	191	11.4	711	7	CO926496
C 40	189.5	11.3	699	8	BZ604233
C 41	183.5	10.9	947	7	CN838521
C 42	182.5	10.9	528	8	BH044856
C 43	182.5	10.9	804	7	CN841612
C 44	177.5	10.6	885	7	CN836251
C 45	176	10.5	681	9	CE066229

#### ALIGNMENTS

RESULT 1	AY403663	893 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY403663				
DEFINITION	Pan troglodytes TMS2R1 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY403663				
VERSION	AY403663.1	GI:39759646			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.				
AUTHORS	1 (bases 1 to 893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
REFERENCE	2 (bases 1 to 893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
SOURCE	1. .893				

